Nucleic Acids, Proteins, and Antibodies

Statement under 37 C.F.R. § 1.77(b)(4)

This application refers to a "Sequence Listing" listed below, which is provided as an electronic document on two identical compact discs (CD-R), labeled "Copy 1" and "Copy 2." These compact discs each contain the following files, which are hereby incorporated in their entirety herein:

Document	File Name	Size in bytes	Date of Creation
Sequence Listing	PJZ02_seqList.txt	2,365,610	01/15/2001
V Viewer Setup File	SetupDLL.exe	695,808	12/19/2000
V Viewer Help File Controller	v.cnt	7,984	01/05/2001
V Viewer Program File	v.exe	753,664	12/19/2000
V Viewer Help File	v.hlp	447,766	01/05/2001

[2] The Sequence Listing may be viewed on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, licensed by HGS, Inc., included on the compact discs (see World Wide Web URL: http://www.fileviewer.com).

Field of the Invention

The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to

these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

- The brain regulates every aspect of human behavior and physiology, from movement, heart rate, blood pressure, and body temperature, to language, emotion, and memories. The prominence of the nervous system among other bodily systems is evidenced by the disproportionate amount of resources consumed by the brain. While comprising only 2% of the body's weight, the brain consumes 20% of the body's oxygen, 25% of the body's glucose, and receives 15% of the cardiac output (see <u>Circulation and energy metabolism of the brain</u>. In: Siegel G, Agranoff B, Albers RW, and Molinoff P, eds. Basic Neurochemistry: molecular, cellular, and medical aspects. 4th ed. New York: Raven Press (1989)).
- The nervous system is organized into the central nervous system (CNS; [5] comprising the brain and spinal cord), and the peripheral nervous system (PNS; comprising the network of nerves that connects the brain and spinal cord to the rest of the body). The basic functional units of the CNS and PNS are neurons, usually composed of dendrites (branching specializations which receive input from other neurons), a cell body (containing the machinery to sustain cellular functions), and an axon (which transmits electrical signals to other neurons or muscle cells). Electrical impulses, propagated along axons by voltagegated ion channels, are converted to chemical signals at junctions between neurons called synapses. Calcium-mediated exocytosis of storage vesicles in the axon terminal leads to neurotransmitter release into the synaptic cleft. The signaling molecules passively diffuse to the postsynaptic membrane and bind to neurotransmitter-specific receptor proteins. Depending on the type of receptor activated, neurotransmitter binding can have a variety of effects on the postsynaptic cell, including activation of second messenger biocehmical cascades and modulation of ion channel permeability. These biochemical and biophysical changes influence the subsequent behavior of the neuron, for example making the cell more or less excitable to incoming signals.

- The elaborate circuitry of the adult nervous system arises through an interaction between genetically programmed growth patterns and environmental influences. During embryonic development, neural connections are formed via the programmed extension of axons under the influence of local molecular cues. Through post-natal development, this coarse pattern of connections is refined based on specific interactions between the child and the environment. It is believed that there are critical periods of neural development in childhood, during which environmental stimulation has a more profound effect on nervous system organization than during adulthood. For example, it is known that sensory deprivation in early childhood (such as blindness or deafness), leads to measurable differences in brain organization (see, for examples, Roder et al., Nature 400(6740):162-6 (1999); Buchel et al., Brain 121 (Pt 3):409-19 (1998)).
- [7] Because of its integral role in human behavior and physiology, disorders of the nervous system are among the most debilitating diseases known. Since the adult nervous system has very limited ability to regenerate, neural injury due to illness or trauma can produce life-long impairments. About half of all spinal cord injuries result in permenant loss of movement and sensation in the arms and legs (quadriplegia). Similarly, up to 30% of stroke survivors are left permanently disabled (American Heart Association 2000 Heart and Stroke Statistical Update, Dallas, TX (1999)). Methods of promoting neural tissue regeneration- for example, to repair spinal cord injuries or brain tissue damage- is a major focus of modern neurobiology. However, currently there is no effective way to repair damaged adult neural tissues.
- [8] A number of neurological conditions, including schizophrenia, depression, and myesthenia gravis, involve impaired or inappropriate synaptic communication between neurons. Drug therapies designed to correct the synaptic chemical imbalances underlying these disorders, such as dopamine receptor antagonists for schizophrenia and serotonin uptake inhibitors for depression, have had varying degrees of success, at the cost of sometimes serious side-effects.
- [9] The immune system is suspected to play a role in some neurological disorders and conditions. For example, multiple sclerosis, which is characterized by sensory impairments (tingling, numbness, dizziness, loss of vision) and motor impairments (tremor, weakness, loss of coordination), is thought to be an autoimmune disorder in which immune cells destroy the insulating myelin sheath covering axons. In addition, the inflammatory immune response can be a serious complication of brain injury (e.g. trauma and stroke),

spinal cord damage, and infection (e.g. encephalitis and meningitis), and may be a common pathological mechanism in many other neurological disorders (Hays, Curr. Pharm. Des. 4:335-48 (1998); Halliday et al., Clin. Exp. Pharmacol. Physiol. 27:1-8 (2000)).

[10] The field of neurobiology is only beginning to uncover the biological basis of neurological diseases. In fact, in most cases the underlying cause or causes remain poorly understood. Thus, the discovery of new human nervous system-associated polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides, satisfies a need in the art by providing new compositions which are useful in the diagnosis, treatment, prevention and/or prognosis of neurological diseases, disorders, and/or conditions, including, but not limited to, neuropsychiatric disorders, neurodegenerative diseases, vascular disorders, developmental disorders, infections, and neoplastic disorders.

Summary of the Invention

The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides

encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", (i.e., nucleotide position numbers) within the polynucleotide provides the location sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIMTM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[13] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third

column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[15] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The

second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[17] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore,

- MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.
- [18] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.
- [19] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.
- [20] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

- [21] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.
- In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.
- [23] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in

column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[24] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC

deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

- In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).
- [26] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.
- [27] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes

at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

- Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.
- [29] Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).
- The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.
- [31] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well

described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADPribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, **GPI** anchor formation, hydroxylation, iodination, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS -STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

- "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1Aor 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.
- [33] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-

polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

- [34] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay nervous system polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 24, 34, 37, 48, and 59.
- [35] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).
- [36] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

TABLE 1A

OMIM	Disease	Reference(s):																		
Cytologic	Band														i de la composition della comp					
Tissue Distribution	Library code: count	(see Table IV for Library	AR061: 0, AR089: 0	L0794: 4, H0039: 2,	S0358: 1, H0013: 1,	H0575: 1, L0770: 1,	L0769: 1 and L0749: 1.		AR089: 15, AR061: 6	H0305: 2			H0135: 1 and H0063:		AR089: 1, AR061: 1	H0052: 1 and T0067:	1			
Predicted Epitopes								His-50 to Leu-69.			Pro-1 to Gly-6,	Ala-41 to Leu-47.			Val-1 to Lys-8,	Pro-36 to Lys-41,	Gln-49 to Lys-57,	Ser-63 to Ser-70,	Asp-79 to Gln-92,	Asn-103 to Thr-122.
AA	SEQ	NO: Y	609					933	610		934		611	935	612					
ORF	(From-To)		1567 - 1148					103 - 309	628 - 227		41 - 187		209 - 361	209 - 361	3 - 410					
SEQ ID	NO: X		11					335	12		336	,	13	337	14					
Contig	ä		1048901					503313	1092566		225905		1198889	507509	522739					
Clone ID NO: Z			HTPAD46 1048901						HCWFF88				HSSAX53		HCEPH71					
Gene	No:								2				3		4					

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AR061: 3, AR089: 2 L0731: 2, H0341: 1, H0392: 1, H0038: 1, H0641: 1, L0803: 1 and H0445: 1.		AR061: 8, AR089: 6 L0439: 5, H0622: 3, H0040: 2, L0794: 2, L0805: 2, L0758: 2, L0803: 1, L0375: 1.	L0659: 1, L0789: 1, L0665: 1, H0579: 1, L0750: 1, L0779: 1, L0777: 1, L0752: 1 and L0755: 1.		AR061: 2, AR089: 1 H0038: 3, L0748: 3, L0659: 2, L0743: 2, L0744: 2, H0486: 1, H0421: 1, H0024: 1, H0031: 1, H0272: 1, L0662: 1, L0384: 1, L0809: 1 and L0779: 1.
Pro-37 to Trp-53, Arg-56 to Pro-62.	Pro-20 to Trp-36, Arg-39 to Pro-45, Gly-62 to Glu-69, Asp-77 to Lys-82, Pro-87 to Ala-93.	Val-21 to Pro-27.		Leu-13 to Val-18, Thr-37 to Lys-46.	Arg-36 to Gln-44, Ser-49 to Gln-57, Lys-276 to Cys-286.
613	936	614		937	615
2 - 970	3 - 575	2 - 1009		2 - 349	149 - 1075
15	338	16		339	17
1083405	522982	1134534		573649	1163883
HTEDF74		HTTEK47			HTOBE75
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	AR061: 1, AR089: 1 H0556: 2, H0634: 1.	L0766: 1 and H0422: 1.									AR089: 7, AR061: 1	H0457: 2, H0529: 2,	H0561: 1, H0521: 1,	S0192: 1 and L0600: 1.					AR089: 3, AR061: 2	H0563: 1 and H0123:		AR089: 16, AR061: 13 H0163: 3 and H0169:	1.		AR061: 9, AR089: 7 H0309: 1
	Leu-21 to Gln-29, Ala-95 to Gly-101,	Arg-163 to Gln-172,	Ser-183 to Glu-202,	Thr-219 to Ser-226,	Thr-231 to Ser-238.	Arg-1 to His-11,	Ser-18 to Gly-27,	Gly-36 to Gly-44,	Asp-97 to Phe-103,	Pro-127 to Gly-132.	Lys-65 to Thr-71,	Lys-104 to Gly-109,	Lys-116 to His-122,	Asn-140 to Asp-146,	Lys-184 to Lys-203,	Glu-205 to Asn-239,	Ala-256 to Phe-267.	Lys-65 to Thr-71.							Pro-19 to Thr-24, Thr-78 to Lys-89.
938	616					939					617							940	618		941	619		942	620
1 - 414	1 - 747		-			2 - 490					69 - 872							70 - 375	475 - 672		129 - 254	341 - 3		162 - 341	767 - 501
340	18					341					19							342	20		343	21		344	22
591896	1156310					592118					1189001							615597	1084887		657020	1017593		685294	1153916
	HCFAT05										HFIAH37								HFTDF15			HPFCU80			HSVAW49 1153916
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	AR089: 2, AR061: 1	L0665: 4, S0132: 2,	L0438: 2, L0439: 2,	L0596: 2, H0542: 2,	H0543: 2, S0114: 1,	H0614: 1, H0592: 1,	H0587: 1, S0280: 1,	H0253: 1, H0581: 1,	H0457: 1, H0012: 1,	H0083: 1, H0687: 1,	H0290: 1, H0622: 1,	H0135: 1, S0150: 1,	L0796: 1, L0646: 1,	L0643: 1, L0764: 1,	L0773: 1, L0649: 1,	L0659: 1, L0663: 1,	H0658: 1, H0555: 1,	H0478: 1, L0752: 1,	L0599: 1 and H0506: 1.		AR089: 3, AR061: 2	H0394: 1 and L0589:					AR089: 89, AR061: 75	S0002: 2, H0521: 2,	S0360: 1, H0123: 1,
Glu-21 to Glu-27.																				Trp-62 to Pro-67.	Phe-16 to Trp-24,	Leu-30 to Val-37,	Phe-41 to Ile-49.	Gln-36 to Ile-46,	Ser-55 to Phe-65,	Ser-67 to Lys-78.	Asn-64 to Pro-73,	Asp-83 to Glu-94,	Leu-144 to Pro-153,
943	621											,								944	622			945			623		
44 - 208	2 - 916																			1 - 627	166 - 342			190 - 456			1527 - 1		
345	23																			346	24			347			25		
689674	1116463							•				1								715096	1065458			723025			1151220		
	HWHQC94 1116463						•	•							,						HRSMD49						HFTDY67		
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S0250: 1, L0654: 1, S0152: 1, L0740: 1 and	L0749: 1.									•	AR089: 1, AR061: 1	S0114: 1, H0583: 1 and	H0013: 1.		AR089: 1, AR061: 1	H0457: 15, H0271: 11,	H0494: 7, H0521: 7,	H0141: 6, H0255: 6,	S0434: 6, L0758: 5,	S0354: 4, S0358: 4,	S0278: 4, H0179: 4,	L0771: 4, L0783: 4,	H0436: 4, H0556: 3,	H0069: 3, H0618: 3,	L0776: 3, L0659: 3,	H0435: 3, H0661: 2,	S0418: 2, S0420: 2,	H0580: 2, S0222: 2,
Glu-162 to Thr-167, Asp-178 to Ser-189.	Gly-197 to Leu-210,	Pro-217 to Pro-222,	Arg-234 to Asp-251,	Gly-279 to Phe-293,	Asp-357 to Gly-367,	Gly-379 to Val-396,	Glu-421 to Met-426,	Asn-441 to Leu-447,	Glu-467 to Trp-474.	Gly-23 to Phe-37.					Glu-18 to Val-28,	Pro-31 to Glu-47,	Glu-88 to Asp-94,	Ser-154 to Lys-178.										
										946	624			947	625													
										1 - 228	247 - 417			246 - 416	3 - 569													
	•									348	26			349	27													
										745221	1090733			786157	1137791													
											HYABL89				HCUEV29													
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H0486: 2, H0013: 2, H0581: 2, H0083: 2, H0266: 2, S0003: 2, H0424: 2, S0036: 2, H0090: 2, H0038: 2	10634: 2, H0616: 2, 30344: 2, S0002: 2, -0770: 2, L0646: 2,	L0662: 2, L0381: 2, L0655: 2, L0809: 2, L0666: 2, L0665: 2.	S0216: 2, H0703: 2, H0547: 2, H0593: 2,	106/0: 2, H0539: 2, 30027: 2, L0748: 2, 0439: 2, 1,0751: 2	L0591: 2, H0543: 2, H0624: 1, H0650: 1.	H0656: 1, S0116: 1, H0484: 1, H0402: 1,	S0376: 1, S0444: 1, S0360: 1, S0045: 1,	S0046: 1, H0619: 1, S6026: 1, H0261: 1,	H0438: 1, H0586: 1, H0559: 1, H0101: 1,	H0427: 1, H0036: 1, F0048: 1, H0318: 1,	S0474: 1, H0421: 1, H0052: 1, H0205: 1,	H0231: 1, L0738: 1,
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H0150: 1, H0081: 1, T0010: 1, H0416: 1, T0006: 1, H0213: 1, H0598: 1, H0135: 1, H0264: 1, H0488: 1, H0623: 1, H0334: 1, H0667: 1, L0773: 1, L0667: 1, L0773: 1, L0667: 1, L0649: 1, L0766: 1, L0649: 1, L0766: 1, L0649: 1, L0766: 1, L0649: 1, L0766: 1, L0636: 1, L0806: 1, L0638: 1, L0806: 1, L0638: 1, L0806: 1, L0638: 1, L0438: 1, S0328: 1, S0052: 1, S0428: 1, H0702: 1, S0428: 1, L0438: 1, S0328: 1, S0146: 1, S0446: 1, S0146: 1, S0446: 1, S0146: 1, S04445: 1, S0026: 1, S0242: 1 and H0576: 1, R0445: 1, S0026: 1, S0242: 1 and	.	AR061: 8, AR089: 5 H0052: 3, S0282: 1, H0194: 1, H0009: 1,
		Glu-1 to Leu-6, Asp-90 to Asp-107.
	948	626
	2 - 298	452 - 72
	350	28
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0602: 1 а		AR061:	L0766: 7,	0731: 7,	0748: 4,	0783: 3,	0418: 2,	0486: 2,	0250: 2,	0763: 2,	0775: 2,	10520: 2,	0752: 2,	0376: 1,	10574: 1,	0414: 1,	H0052: 1,	10014: 1,	, H0688: 1,	H0623: 1,	10529: 1,	,0761: 1,	,0809: 1,	,0665: 1,	[0684: 1,	0390: 1,	,0745: 1,
L0789: 1, L0602: 1 and L0439: 1.		AR089: 3, AR061:	S0358: 8, L0766: 7,	.0777: 7, L0731: 7	.0659: 4, L0748: 4,	.0751: 4, L	.0663: 3, S0418: 2	S0360: 2, H0486: 2,	0010: 2, S	0422: 2, L	.0803: 2, L	.0789: 2, E	.0756: 2, L	10656: 1, S	10208: 1, F	10632: 1, S	10581: 1, F	H0024: 1, H0014: 1,	H0355: 1, F	H0090: 1, H0623:	10509: 1, I	.0520: 1, L	.0650: 1, I	L0666: 1, L0665: 1	0126: 1, E	H0648: 1, S0390:	L0740: 1, L0745: 1
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	Thr-21 Ile-91.	r-6,	Glu-91																								
	Asp-15 to Thr-21, Gln-83 to Ile-91.	Ile-1 to Ser-6,	Leu-81 to Glu-91.																								
	949	627																			-						
	7 - 512) - 502																	· .								
	147	230 -								***																	
	351	29																									
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L0749: 1, L0750: 1, L0755: 1, L0591: 1, L0362: 1 and S0242: 1.	T	AR089: 1, AR061: 0	S0222: 1, S0002: 1, L0804: 1, L0663: 1 and H0521: 1.	AR089: 30, AR061: 8	S0044: 2, L0748: 2,	L0770: 1 and H0519: 1.	F		AR089: 163, AR061:	32	H0618: 1, L0368: 1	and S0053: 1.	AR089: 15, AR061: 5	L0754: 5, L0755: 5,	S0354: 3, L0483: 3,	H0648: 3, L0777: 3,	S0374: 2, L0751: 2,	L0758: 2, L0605: 2,	L0362: 2, H0543: 2,	S0114: 1, S0358: 1,	H0411: 1, H0575: 1,	L0105: 1, H0263: 1,	H0596: 1, H0510: 1,
		Phe-7 to Pro-15,	1 Tp-34 to Gly-40.	Met-1 to Ser-8.			Lys-1 to Asp-7,	Gln-47 to Arg-53.	Val-47 to Gly-65.				Gln-24 to Thr-32,	Ser-154 to Phe-163.									
	950	628		629			951		630				631										
	222 - 494	2 - 685		862 - 619			11 - 178		2 - 307				3 - 608										
	352	30		31			353		32				33										
	839777	846624		1052388			867287		870247				1152279										
		HDPBS64		HTBAB41					HTLGE31				HWLHK29										
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H0169: 1, H0090: 1, H0059: 1, S0440: 1, L0373: 1, L0372: 1, L0800: 1, L0662: 1, L0794: 1, L0649: 1, L0803: 1, L0804: 1, L0659: 1, L0783: 1, L0790: 1, L0783: 1, L0790: 1, L0783: 1, L0790: 1, L0789: 1, L0665: 1, S0378: 1, L0665: 1, S0378: 1, L0665: 1, S0378: 1, S0446: 1, S0196: 1 and S0446: 1.		AR089: 2, AR061: 1 S0360: 1, H0013: 1, L0664: 1 and H0542: 1.		AR089: 1, AR061: 1 H0046: 34, L0731: 5, L0534: 4, L0769: 4, H0521: 4, S0356: 3, L0800: 3, L0794: 3, L0439: 3, L0749: 3, L0752: 3, L0759: 3, L0562: 2, H0486: 2, L0803: 2, L0805: 2,
E	Gln-18 to Thr-26.	Arg-4 to Glu-12, Glu-121 to Gly-126, Ala-141 to Pro-146, Gln-161 to Phe-176, Lys-186 to Ser-194.		Pro-1 to Gly-7, Val-127 to Val-133, Leu-162 to Ser-171, Arg-178 to Glu-185, Pro-195 to Thr-200, Gln-243 to Trp-248, Gln-252 to Asn-265, Glu-313 to Cys-319, His-417 to Glu-422,
	952	632	953	633
	3 - 491	3 - 971	26 - 820	1 - 2460
	354	34	355	35
	876064	1106816	894409	1217035
	- 1	HHEGG20		HDPRU43
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L0809: 2, L0789: 2, L0744: 2, L0485: 2, H0556: 1, H0657: 1, H0637: 1, H0580: 1, H0609: 1, H0261: 1, H0609: 1, H0455: 1, H0609: 1, H0586: 1, H0618: 1, H0544: 1, H0618: 1, H0544: 1, H0620: 1, H0569: 1, H0620: 1, H0688: 1, H0252: 1, H0688: 1, H0252: 1, H0688: 1, H0252: 1, H0668: 1, L0639: 1, L0771: 1, L0639: 1, L0771: 1, L0659: 1, L0771: 1, L0655: 1, H0699: 1, H0660: 1, L0773: 1, L0655: 1, H0699: 1, L0655: 1, H0699: 1, L0655: 1, L0777: 1, L0658: 1, L0777: 1, L0658: 1, L0777: 1,		AR089: 6, AR061: L0754: 6, L0777: 6, L0740: 5, L0731: 4, L0758: 4, L0759: 4,
Arg-464 to Ala-473, Met-530 to Lys-538, Arg-594 to Gly-599, Glu-641 to Gly-649, Asp-660 to Ala-668, Arg-705 to Ser-727, Ser-777 to Glu-783, Leu-796 to Gly-806.	Pro-8 to Gln-16.	Val-30 to Ser-37.
	954	634
	1 - 342	2 - 367
	356	36
	909841	1227647
		HE8PK12
		26

S0001: 3, S0280: 3, L0770: 3, L0764: 3, L0770: 3, L0749: 3, L0366: 3, S0412: 3, S0007: 2, H0411: 2, H0013: 2, L0471: 2, T0004: 2, L0598: 2, L0783: 2, L0662: 2, L0783: 2, L0744: 2, L0748: 2, L0779: 2, L0748: 2, L0779: 2, L0752: 2, H0170: 1, S0282: 1, H0662: 1, H0427: 1, H0590: 1, S0049: 1, H0194: 1, H0553: 1, S0306: 1, L076: 1, L0163: 1, L076: 1, L0163: 1, L076: 1, L0659: 1, L0526: 1, L0809: 1, L0526: 1, L0809: 1, L0652: 1, L0648: 1, H0572: 1, L0743: 1,	L0/80: 1, S0031: 1, H0343: 1, L0604: 1 and H0653: 1.	
	<u> </u>	Val-30 to Ser-37,
		955
		2 - 367
		357
		909884
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	AR061: 1, AR089: 0 L0439: 3, H0616: 2,	: 1, H0013: 1,	H0590: 1, S0010: 1, H0046: 1, H0050: 1,	i: 1, H0615: 1,	S0366: 1, H0529: 1, H0144: 1, S0126: 1	S0152: 1, S3014: 1 and			1: 1, AR089: 0	S0040: 1, H0580: 1,	S0222: 1, H0355: 1,	S0250: 1, L0565: 1 and	-:										
	AR061: L0439: 1 0749: 2	H0415	H059C H0046	H0375	S0366 H0144	S0152	L0779: 1.		AR061:	S004	S0222	S0250	S0152: 1										
Gln-43 to Asp-62, Pro-74 to Glu-79, Thr-102 to Phe-109.	Asn-2 to Gly-10, Asp-86 to Ile-110,		Ala-16/ to Ser-1/2, Leu-176 to Lys-183.					Thr-1 to Gly-9.	Tyr-83 to Ser-92,	Leu-118 to Tyr-123,	Leu-137 to Ser-143,	Gln-148 to Ser-158,	Thr-258 to Pro-266,	Gln-274 to His-283,	Asp-325 to Ser-334,	Gln-343 to Thr-349,	Ser-366 to Val-378,	Arg-381 to Asp-388,	Pro-426 to Asn-431,	Cys-446 to Ser-457,	Leu-469 to Lys-486,	Cys-501 to Arg-510.	Gly-1 to Trp-6.
	635		,					926	989														957
	1 - 1050							2 - 1048	578 - 2143														1 - 429
	37							358	38														359
	1227519							911510	1217059				,										911566
	НЕ9НV92								HOHCE47												<u></u>		
	27								28														

AR061: 6, AR089: 5 H0328: 4, H0031: 3, L0519: 3, L0748: 2, L0777: 2, L0731: 2, S0260: 2, H0624: 1, S6024: 1, H0650: 1, S0116: 1, H0254: 1, H0441: 1, H0438: 1, H0574: 1, H0156: 1, H0599: 1, S0051: 1, H0599: 1, S0051: 1, L0564: 1, L0763: 1, L0766: 1, L0774: 1, L0766: 1, L0774: 1, L0766: 1, L0774: 1, L0766: 1, L0774: 1, L0766: 1, L0659: 1, L0776: 1, L0659: 1, L0666: 1, L0663: 1, S0242: 1 and H0423: 1.	· _T	AR089: 1, AR061: 1 L0794: 4, L0438: 4, L0761: 3, L0766: 3, L0748: 3, L0439: 3, H0556: 2, L0602: 2, L0754: 2, L0779: 2, H0580: 1, H0208: 1, H0013: 1, T0082: 1, S0010: 1, H0428: 1,
His-13 to Gly-21, Tyr-61 to Asp-66, Ala-105 to Thr-110.	His-13 to Gly-21, Tyr-61 to Asp-66, Ala-105 to Thr-110.	Leu-15 to Ser-21, Leu-89 to Tyr-94, Gly-130 to Gln-136, Asn-163 to Leu-168, Lys-176 to His-181, Ile-187 to Arg-193, Ala-239 to Thr-244, Pro-263 to Val-268, Ala-401 to Ser-406.
637	958	638
74 - 412	202 - 540	3 - 2840
36	360	40
1154067	917180	1227639
HSD[[69		HKAKM10
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H0553: 1, H0038: 1, H0616: 1, H0494: 1, L0796: 1, L0800: 1, L0773: 1, L0533: 1, L0803: 1, L0776: 1, L0657: 1, L0791: 1, H0520: 1, H0519: 1, H0521: 1, H0187: 1, L0731: 1, S0031: 1 and L0366: 1.				AR061: 6, AR089: 5			-							- `	AK089: 1, AK061: 0	H0056: 3, H0437: 1, H0050: 1 and S0002: 1.	AR089: 27, AR061: 11
	Gly-25 to Gln-31, Asn-58 to Leu-63,	Lys-71 to His-76, le-82 to Arg-88,	Ala-134 to Thr-139.	Lys-65 to Thr-71,	Lys-104 to Gly-109,	Lys-116 to His-122,	Asn-140 to Asp-146,	Lys-184 to Lys-203,	Glu-205 to Asn-239,	Ala-230 to Pne-20/.	Lys-16 to Thr-22,	Lys-55 to Gly-60,	Lys-67 to His-73,	Asn-91 to Asp-97.			
	959			639						***************************************	096			010	040		641
	2 - 547			1037 - 1840						- 1	219 - 593			100	125 - 355		88 - 435
	361			41							362				47		43
	918685			1226120							920347			000	928054		928344
				HCEPU56										\neg	HUSHB54		HLMD095
				31											32		33

10250: 2, 1216: 2, 0638: 1, 0416: 1, 1776: 1, 1 S0052: 1.	AR061: 7 S0438: 2, 5015: 1, 0393: 1, 0355: 1, 0144: 1, 0750: 1,		AR051: 29, AR050: 24, AR054: 18, AR089: 1, AR061: 0 T0082: 1, T0023: 1 and L0596: 1.	- 1	AR089: 2 L0666: 2, 0777: 2, .0021: 1, 10688: 1,
H0271: 3, H0250: 2, H0635: 2, S0216: 2, H0254: 1, H0638: 1, H0069: 1, H0416: 1, H0090: 1, L0761: 1, L0800: 1, L0776: 1, L0789: 1 and S0052:	AR089: 21, AR061: H0510: 3, S0438: 2, L0803: 2, L0615: 1, S0418: 1, H0393: 1, H0632: 1, H0355: 1, L0774: 1, H0144: 1, L0749: 1, L0750: 1, L0605: 1 and L0581:		AR051: 29, 24, AR054: 1, AR061: T0082: 1, T0596: 1.		AR061: 3, AR089: 7 L0758: 3, L0666: 2, L0751: 2, L0777: 2, H0663: 1, L0021: 1, H0309: 1, H0688: 1, H0617: 1, H0477: 1,
	Gly-1 to Gly-6, Arg-12 to Arg-17, Gln-56 to Ser-71, Glu-82 to Glu-89, Phe-94 to Glu-104, Ala-126 to Asn-131, Pro-167 to Gly-177, Thr-224 to Ala-233, Leu-237 to Lys-281.	Gly-1 to Gly-6, Arg-12 to Arg-17.			Ser-1 to Gly-23, Gly-85 to Leu-91.
	642	961	643	962	644
	50 - 892	40 - 855	3 - 548	181 - 768	501 - 803
	44	363	45	364	46
	1198902	928730	1164340	933441	1152268
	HHASQ32 1		HARAB87		HTNGF69
	34		35		36

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L0766: 1, L0775: 1, L0367: 1, L0789: 1, L0663: 1, L0438: 1, L0749: 1, L0779: 1, L0757: 1 and S0456: 1.		AR054: 16, AR051:	15, AK050: 12, AK089: 0. AR061: 0	L0777: 6, L0758: 5,	L0779: 4, L0803: 3,	S0358: 2, H0004: 2,	L0662: 2, L0775: 2,	H0144: 2, S0126: 2,	S0328: 2, S3014: 2,	S0027: 2, L0743: 2,	L0748: 2, H0265: 1,	H0656: 1, S0212: 1,	H0663: 1, H0638: 1,	H0580: 1, H0632: 1,	H0486: 1, H0599: 1,	H0618: 1, L0105: 1,	H0251: 1, H0309: 1,	H0544: 1, H0123: 1,	H0050: 1, L0471: 1,	H0024: 1, H0399: 1,	S0003: 1, H0364: 1,	H0553: 1, H0038: 1,	H0412: 1, H0413: 1,
	Ser-1 to Gly-23, Gly-85 to Leu-91.	Thr-15 to Arg-22,	Ala-38 to Met-43, Gln-49 to Lys-64.	Thr-97 to Gln-108,	~`	•		Ser-379 to Ala-386,	Asp-402 to Ser-417,		Arg-443 to Gly-459,												
	963	645																					
	483 - 785	1 - 1461																					
	365	47																					
	933614	1154788																					
		HMSJL96																					
		37																				· · · · ·	

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T0041: 1, S0344: 1, S0002: 1, L0598: 1, H0529: 1, L0645: 1, L0804: 1, L0804: 1, L0806: 1, L0558: 1, L0792: 1, L0792: 1, L0666: 1, S0374: 1, H0555: 1, S0374: 1, H0555: 1, S0206: 1, S0032: 1, L0439: 1, L0757: 1, S0192: 1, H0707: 1, S0192: 1, H0708: 1.		AR089: 2, AR061: 1 L0754: 6, H0318: 3, H0486: 2, H0014: 2, L0777: 2, H0543: 2, H0171: 1, S6024: 1, H0650: 1, S0354: 1, H0455: 1, H0013: 1, L0483: 1, H0494: 1, S0450: 1, L0520: 1, L0763: 1, L0769: 1,
	Thr-15 to Arg-22, Ala-38 to Met-43, Gln-49 to Lys-64, Thr-97 to Gln-108, Thr-131 to Lys-137.	
	964	646
	1 - 426	3 - 905
	366	48
	934483	1205261
		HDTBT06
		38

L0641: 1, L0521: 1, L0662: 1, L0774: 1, L0776: 1, L0783: 1, L0663: 1, S0136: 1, H0478: 1, L0742: 1, L0439: 1, L0780: 1, L0592: 1, S0192: 1 and S0424: 1.		AR061: 4, AR089: 4	L0615: 1, S0420: 1, H0333: 1, H0286: 1,	H0634: 1 and H0144: 1.									AR089: 5, AR061: 5	L0748: 2, L0749: 2,	H0085: 1, H0050: 1,	H0090: 1 and L0758: 1.	AR089: 12, AR061: 7	H0583: 1, H0675: 1	and H0457: 1.	
		Thr-8 to Ser-16,	Arg-34 to Leu-42, Thr-46 to Glu-51,	Thr-57 to Arg-66,	Gln-94 to Ala-100,	301-12/ to Old-134.	Thr-6 to Ser-14,	Arg-32 to Leu-40,	Thr-44 to Glu-49,	Thr-55 to Arg-64,	Gln-92 to Ala-98,	Ser-125 to Glu-132.	Cys-9 to Arg-14,	Arg-21 to Gly-28.						Gly-8 to Ile-13, Glu-141 to His-146,
	965	647					996						648				649			296
	1 - 906	2 - 574					1 - 567						825 - 253				562 - 2			139 - 921
	367	49				0,0	368						20				51			369
	935404	1165363					941834						946668			-	1083553		-	949062
		HTTIE47											HHFBP47				HCCCC81			
		39											40				41			•

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-	AR089: 7, AR061: 6	H0521: 2, H0039: 1,	H0641: 1, H0529: 1,	L0654: 1, H0701: 1,	H0518: 1, S0152: 1 and	H0522: 1.					AR061: 1, AR089: 0	L0758: 4, L0617: 2,	L0794: 2, H0253: 1,	H0038: 1, H0616: 1,	L0789: 1 and L0779: 1.							AR089: 1, AR061: 0	L0759: 4, L0770: 2,	S0040: 1, S0318: 1,	S0334: 1, S0316: 1,	S0340: 1, H0038: 1,	L0598: 1, L0800: 1 and	S0276: 1.
Glu-186 to Glu-195, Asn-213 to Asn-218	Gln-49 to Pro-66,	Ser-96 to Thr-108,	Glu-116 to Glu-135,	Arg-140 to Pro-152,	Ser-167 to Arg-172,	Pro-175 to Leu-185,	Ala-199 to Lys-215,	Pro-228 to Leu-237,	Pro-247 to Ser-253.	Ser-5 to Gly-20.	Glu-13 to Asp-29,	Glu-50 to Lys-58,	Thr-61 to Glu-66,	Ala-94 to Tyr-100,	Gln-146 to Ser-156,	Pro-171 to Asp-177,	lle-179 to Trp-191,	Glu-197 to Val-203,	Asp-238 to Lys-244,	Pro-304 to Ala-315.	Glu-13 to Thr-27.							
	650									896	651										696	652						
	976 - 164									269 - 2029	43 - 1143	-									42 - 443	510 - 208						
	52									370	53										371	54						
	1197841									949153	1136121										953803	954614						
	HPJEV71										HTEIL07											HTEAG49	·					
	42										43											44			-			

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									-	:	••											-						
AR054: 38, AR050:	26, AR051: 25, AR061:	2, AR089: 1	S0028: 1							AR051: 23, AR050:	14, AR061: 10, AR054:	4, AR089: 3 S0053: 1			AR089: 1, AR061: 1	H0031: 2		AR061: 1, AR089: 0	H0556: 2, L0756: 2,	H0423: 2, S0134: 1,	H0580: 1, H0271: 1,	T0006: 1, H0264: 1,	H0560: 1, H0641: 1,	S0142: 1, L0805: 1,	L0809: 1, L0789: 1,	H0555: 1, L0780: 1 and	S0031: 1.	AR089: 14, AR061: 10
		Gln-20 to Gly-25,		Pro-134 to Asp-139,	Asn-164 to Thr-171	Pro-223 to Arg-228.	Thr-1 to Cys-6,	Ser-52 to Gly-57,	Gln-111 to His-117.	Lys-17 to Thr-23,	His-95 to Thr-101.		Lys-17 to Thr-23.	His-95 to Thr-101.			Met-43 to Trp-52.	Ser-1 to Ser-6,	Thr-14 to Gly-28.									His-14 to Gly-19,
653							970			654			971	1	655		972	959										657
355 - 1248							1332 - 430			183 - 593			963 - 553		191 - 391		191 - 346	3 - 1091					-					410 - 988
55							372			56			373)	57		374	58										59
637670							954777			861673			056105	20100	1050684		695656	959622				-				-		1197898
HSLCF96										HNHCI32					HPMFL08			HTXRA13										HCE3H71
45										46					47		-	48										49

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L0439: 12, L0438: 5, L0741: 4, H0052: 2, H0009: 2, L0769: 2, L0794: 2, H0229: 1, H0572: 1, L0770: 1, L0796: 1, L0789: 1 and L0786: 1.		AR089: 0, AR061: 0	S0464: 1 and L0356: 1.				AR089: 4, AR061: 1	H0038: 2, H0556: 1,	H0341: 1 and L0596: 1.										AR061: 5, AR089: 2	H0154: 2			JAR061: 1, AR089: 0
Pro-21 to Pro-28, Arg-49 to Gln-54, Pro-82 to Pro-91, Gly-102 to Ser-108, Arg-150 to Ser-155, Pro-160 to Asn-168, Ala-175 to Glu-188.		Pro-4 to Glu-13,	Asn-23 to Arg-29,	Gln-91 to Arg-100.	Glu-1 to Glu-6,	Asn-16 to Arg-22.	Arg-1 to Ser-12,	Leu-33 to Leu-40,	His-42 to Phe-49,	Glu-51 to Met-57,	Gly-72 to Phe-78.	Val-3 to Tyr-15,	Leu-17 to Thr-27,	Ser-34 to Ser-61,	Leu-82 to Leu-89,	His-91 to Phe-98,	Glu-100 to Met-106,	Gly-121 to Phe-127.	Arg-1 to Ser-8,	Lys-42 to Lys-48.	Arg-1 to Ser-8,	Lys-42 to Lys-48.	Pro-38 to Lys-43,
	973	658			974		659					975							099		926		661
	275 - 826	3 - 323			3 - 302	********	1 - 549					32 - 523							152 - 295		147 - 332		165 - 662
	375	09			376		61					377							62		378		63
	961681	1134914		•	966029		1021235					530595			-				1153913		573345	_	1182286
	1	HUTSF11					HTEGI48												HSFAM09				HNFHK77
		50					51												52				53

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H0271: 2		AR089: 1, AR061: 1 S0001: 3		AR051: 4, AR054: 1,	AR089: 1, AR061: 0,	AR050: 0	S0046: 1, S0028: 1, S0031: 1 and S0260: 1.								AR089: 5, AR061: 3	S0250: 4, L0745: 2,	H0393: 1, H0587: 1,	L0744: 1, L0748: 1,	L0439: 1 and L0752: 1.							AR061: 4, AR089: 2
Glu-126 to Tyr-132, Trp-161 to Arg-166.	Pro-38 to Lys-43.		Arg-1 to Cys-10.		Ile-64 to Arg-69,	Asn-142 to Pro-147,	Pro-349 to Asp-356.	Leu-6 to Pro-11,	Ile-66 to Arg-71,	Asn-144 to Pro-149,	Pro-351 to Asp-358.	Ile-57 to Arg-62,	Asn-135 to Pro-140,	Pro-342 to Asp-349.		Glu-41 to Ser-53,	Arg-67 to Ser-72,	Asn-111 to Arg-122,	Gly-212 to Arg-218,	Gln-229 to Ser-235,	Arg-239 to Lys-244.	Ser-4 to Arg-9,	Glu-41 to Ser-53,	Arg-67 to Ser-72,	Asn-111 to Arg-122.	Lys-79 to Asp-87,
	716	662	876	663				626	•			086			664							981				665
	165 - 422	12 - 608	16 - 207	1 - 1068				2 - 1075	•			1595 - 549			2 - 1003							2 - 478				2 - 718
	379	64	380	65				381				382			99							383				29
	576186	1012602	578847	1104406		-		587311				954821			1199645			-				676214				1082367
	. .	HFXDO83		HSDIW73				•							HFVGD23											HMSBZ24
		54		55	-										56											57

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H0331: 1, S0002: 1, H0519: 1 and L0741: 1.		AR089: 1, AR061: 1	LU8U3: 3, SU3S4: 2,	H0052: 2, H0617: 2, I 0770: 2 I 0646: 2	S0028: 2, L0753: 2,	H0445: 2, H0556: 1,	S6024: 1, H0657: 1,	S0418: 1, S0420: 1,	H0351: 1, H0441: 1,	H0586: 1, H0013: 1,	S0280: 1, H0156: 1,	L0021: 1, H0122: 1,	S0010: 1, H0571: 1,	L0163: 1, H0135: 1,	H0412: 1, H0100: 1,	L0351: 1, L0769: 1,	L0639: 1, L0764: 1,	L0649: 1, L0659: 1,	L0809: 1, L0530: 1,	H0520: 1, H0547: 1,	H0519: 1, H0690: 1,	H0539: 1, S0136: 1,	H0696: 1, L0748: 1,	L0747: 1, L0756: 1,	L0779: 1, L0757: 1,	S0434: 1, S0436: 1,	S0011: 1 and H0136: 1.
Lys-100 to Asp-106.		Thr-1 to Ser-10,	Ala-/3 to 1yr-80, $A = 123 + 12$	Arg-133 to Ser-143, Glv-174 to His-179	Ser-201 to Arg-224,	Asn-236 to Gly-241,	Tyr-260 to Cys-272,	Pro-274 to Thr-284,	Gln-292 to Glu-306,	Cys-409 to Arg-414,	Arg-424 to Arg-432,	Asp-523 to His-531,	Thr-552 to Pro-557,	Asn-601 to Pro-606,	His-612 to His-618,	Pro-678 to His-684,	Asn-698 to Gln-705.										All a services
-	982	999																									
	2 - 322	3 - 2186																									
	384	89																									
	678707	1217042																									
		НЖННВ69															•				-						
		58																									

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							;																	
	AR061: 1, AR089: 1 H0052: 2 H0135: 2	S0282: 1, H0254: 1,	H0051: 1, H0634: 1,	S0152: 1, H0436: 1 and	H0677: 1.		-	AR089: 16, AR061: 8	S0038: 2, H0438: 1, S0049: 1 and H0547: 1			AD080- 4 AD061- 3		T0010: 1 and H0604: 1.		AR089: 14, AR061: 6	H0555: 1 and L0777:	•		AR061: 6, AR089: 3	L0758: 2, S0222: 1,	H0038: 1 and H0539: 1.		
Gly-1 to Ser-7.	Gly-49 to Gly-60, Arg-84 to Cvs-97	Pro-100 to Gln-106,	Ala-113 to Ala-137,	Ala-145 to Trp-156,	Ala-172 to Tyr-182,	Asn-218 to Tyr-225.		Ser-1 to Ser-12,	Arg-33 to Arg-50, Tvr-117 to Leu-125.	Gln-3 to Ser-12,	Arg-33 to Arg-50,	20.000				Lys-1 to Leu-6,	Asp-25 to Pro-30.	I via 1 to I air 6	Asp-25 to Pro-30.	Leu-59 to Thr-82,	Lys-89 to Gly-94,	Gln-155 to Val-161,	Lys-169 to Ala-179.	Gln-6 to Lys-14, Leu-68 to Glu-90.
983	<i>L</i> 99						984	899		985		660			986	0/9		700	706	671				886
1 - 261	626 - 91						3 - 230	124 - 588		124 - 456		2 131	•		3 - 434	2 - 472		- 1	7/4-7	61 - 597				3 - 482
385	69					,	386	70		387		7.1	1,		388	72		700	209	73				390
690442	1162543						692773	1156765		706115		1140408	07+0+11		715899	1148046	<u>-</u>	717750	/1/330	1153918				723446
	HFXLC69							HBXBW40 1156765		•		UCE11 51				HRADM45		•		HTEF045				
	59							09				7	5			62				63				

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AR089: 1, AR061: 0	S0002: 2, H0521: 2,	S0360: 1, H0123: 1,	S0250: 1, L0654: 1,	S0152: 1, L0740: 1 and	L0749: 1.																AR089: 1, AR061: 0	L0776: 5, L0764: 4,	L0743: 4, L0740: 3,	L0750: 3, L0777: 3,	L0731: 3, S0001: 2,	H0438: 2, H0052: 2,	H0194: 2, H0201: 2,	L0526: 2, H0144: 2, L0742: 2, H0662: 1,
Asn-41 to Pro-50,	Asp-60 to Glu-71,	Leu-121 to Pro-130,	Glu-139 to Thr-144,	Asp-155 to Ser-166,	Gly-174 to Leu-187,	Pro-194 to Pro-199,	Arg-211 to Asp-228,	Gly-256 to Phe-270,	Asp-334 to Gly-344,	Gly-356 to Val-373,	Glu-398 to Met-403,	Asn-418 to Leu-424,	Glu-444 to Trp-451,	Cys-465 to Tyr-474.	Asn-41 to Pro-50,	Asp-60 to Glu-71,	Leu-121 to Pro-130,	Glu-139 to Thr-144,	Asp-155 to Ser-166,	Gly-174 to Asp-188.	Lys-1 to Ala-6,	Ser-38 to Gln-43,	Pro-88 to Ala-112,	Pro-141 to Asp-148,	Gly-186 to Thr-200,	Pro-231 to Ala-238,	Leu-248 to Ser-254.	
672															686						673							,
2 - 1465				-			<u>-</u>								3 - 629						834 - 1							
74															391						75							
1152271													•		724322						1217026							
HOHBN82 1152271																					HWHGF52							
64																					9							

H0619: 1, H0261: 1, H0392: 1, H0455: 1, H0586: 1, H0587: 1, H0574: 1, H0486: 1, S0010: 1, S0346: 1, T0110: 1, H0009: 1, L0157: 1, H0320: 1, H0604: 1, H0163: 1, H0646: 1, L0763: 1, L0638: 1, L0630: 1, L0651: 1, L0523: 1, L0651: 1, L0666: 1, L0663: 1, L0666: 1, L0663: 1, L0666: 1, L0663: 1, L0664: 1, H0547: 1, H0660: 1, S0404: 1, L0744: 1, L0439: 1, L0752: 1,		AR089: 1, AR061: 0 S0364: 3, S0366: 3, L0604: 3, H0624: 1, L0622: 1, L0623: 1, H0041: 1, L0791: 1, S0380: 1 and L0748: 1.
	Gln-1 to Lys-8, Gly-10 to Trp-17, Val-28 to Gly-43, Thr-54 to Glu-63.	
	066	674
	1 - 453	1115 - 321
	392	76
	726102	1223861
		HBKDI30
		99

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	AR061: 4, AR089: 2 H0650: 2, H0052: 2, H0547: 2, H0542: 2, S0212: 1, S0222: 1, T0114: 1, L0483: 1, H0628: 1, L0455: 1, H0413: 1, S0344: 1, L0766: 1, L0775: 1, L0805: 1, L0665: 1, H0520: 1, H0519: 1, S0126: 1, H0521: 1, S0044: 1, S0390: 1, L0592: 1 and S0026: 1.		AR061: 2, AR089: 1 S0010: 1, H0135: 1, L0766: 1, L0745: 1, L0779: 1 and L0758: 1.		AR061: 2, AR089: 1 S0282: 1 and S0051: 1.		AR089: 2, AR061: 2 S0002: 2
Gly-15 to Thr-21, Glu-76 to Lys-86.	Ser-116 to Asp-125, Glu-183 to Ser-188, Arg-228 to Gln-234, Leu-280 to Lys-303.	Glu-41 to Ser-46.	Pro-2 to Gly-10.	Asp-52 to Leu-57, Lys-82 to Thr-87, Ser-90 to Trp-98, Ser-118 to Leu-123.	His-13 to Asn-24.		Ser-11 to Ser-21, Ser-84 to Ala-89, Pro-98 to Arg-107.
991	675	992	929	993	<i>LL</i> 9	994	829
1 - 381	1 - 1170	2 - 319	1 - 735	115 - 633	563 - 985	2 - 325	1 - 411
393	77	394	78	395	79	396	80
729048	1185143	730964	1102593	732597	1220851	743166	746582
	HSQFR54		HAGBA56		HHSAE29		HMSHO64
	29		89		69		70

AR061: 4, AR089: 2 S0222: 1, S0280: 1, L0774: 1, L0376: 1 and S0378: 1.		AR061: 2, AR089: 1	L0752: 3, L0747: 2,	H0294: 1, H0253: 1,	H0046: 1, H0040: 1,	HU005: 1, HU494: 1,	S0352: 1, L0/69: 1,	L0766: 1, L0804: 1,	L0805: 1, L0791: 1,	H0521: 1, L0779: 1,	L0780: 1, L0731: 1 and	L0758: 1.		AR089: 0, AR061: 0	H0520: 1	-						AR089: 1, AR061: 1	H0052: 1 and H0194:	:	
Lys-1 to Ala-6, Ala-17 to Leu-25, Arg-54 to Ala-59, Val-61 to Arg-66, Ser-90 to Gly-95.		Lys-31 to Ala-48,	Gln-51 to Thr-62,	Gln-105 to Ser-110,	Cys-126 to Leu-134,	GIN-13/ 10 GIY-130,	His-174 to Ala-205,	Arg-212 to Pro-220,	Pro-227 to Gly-232,	Gly-245 to Ala-251,	Ala-257 to Ser-263,	Leu-266 to His-283.		Pro-1 to Glu-6,	His-17 to Lys-22,	Pro-52 to Gln-58,	Gly-123 to Arg-130,	His-205 to Ala-210.	Pro-1 to Glu-6,	His-17 to Lys-22,	Pro-52 to Gln-58.				
629	995	089											966	681					766			682		800	770
762 - 376	224 - 619	2886 - 2005	-										1 - 282	2 - 679					2 - 688			105 - 326		105 276	102 - 270
81	397	82											398	83					399			84		001	400
154786	750631	1224371											751985	1143523					757184			1183334		1/1001	/01881
HFPBW22 1154786	L	HTLBH67												HNTMH70								HCETC59			
71		72												73								74			

																			,										
AR061: 1, AR089: 1	H0539: 4, L0439: 4,	L0438: 2, H0013: 1,	L0758: 1 and L0592: 1.																AR089: 33, AR061: 18	L0748: 2 and H0253:	<u></u>							AR061: 13, AR089: 5	L0805: 2, H0436: 2,
Asp-8 to Ala-13,	Ala-26 to Arg-33,	Pro-38 to Ala-50,	Pro-60 to Asn-65,	Asp-68 to Ser-74,	Arg-109 to Arg-132,	Asp-140 to Leu-145,	Ala-149 to Ser-154,	Ile-158 to Asp-169,	Glu-171 to Ala-177,	Cys-213 to Pro-218,	Pro-226 to Lys-231,	Thr-244 to Phe-249,	Arg-361 to Ile-370.	Arg-39 to Arg-62,	Asp-70 to Leu-75,	Ala-79 to Ser-84,	Ile-88 to Asp-99,	Glu-101 to Ala-10/.	His-1 to Thr-6,	Arg-30 to Thr-35,	Lys-40 to Ala-71,	Pro-209 to Glu-222,	Arg-231 to Tyr-237,	Pro-239 to Tyr-245,	Arg-263 to Ala-271,	Gln-290 to Trp-306.	Ala-1 to Ala-35.	Asp-44 to Ile-50,	Arg-121 to Leu-132,
683														666					684								1000	685	
2 - 1237		-		•										214 - 798					3 - 947								90 - 422	2 - 523	
85								-						401					98								402	87	
1161223														767871					1136124		•						772363	1124695	
HE8UX76 1161223																			HTLEN77									HBGDI80 1124695	
75																			9/	-								77	

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L0439: 2, L0362: 2, S0358: 1, L0483: 1, H0181: 1, S0422: 1, L0369: 1, L0804: 1, L0787: 1 and L0663: 1.		AR061: 2, AR089: 2	L0777: 3, L0794: 2, S0027: 2, 1,0748: 2.	L0747: 2, L0601: 2,	S0342: 1, S0212: 1,	S0282: 1, L0004: 1,	S0045: 1, H0581: 1,	T0110: 1, L0471: 1,	S6028: 1, H0551: 1,	H0494: 1, H0509: 1,	L0646: 1, L0665: 1,	H0520: 1, H0547: 1,	S0390: 1, L0591: 1,	L0366: 1 and H0653: 1.					-				
Lys-148 to Ser-160.	Asp-13 to Ile-19, Pro-37 to Arg-42.	Gln-1 to Thr-7,	Glu-28 to Gln-35,	Ser-238 to Gly-245.	Asp-278 to Gly-283,	Pro-317 to Ser-324,	Ser-335 to Glu-342,	Pro-344 to Lys-355,	Glu-362 to Asn-373,	Glu-385 to Arg-393,	Arg-399 to Gln-417,	Lys-422 to Gln-457,	Glu-461 to Glu-477,	Leu-514 to Glu-529,	Leu-538 to Met-548,	Gln-562 to Gln-567,	Asn-569 to Asp-574,	Arg-594 to Gln-609,	Asn-626 to Met-636,	Ala-638 to Lys-649,	Glu-654 to Gln-670,	Gln-676 to Leu-716,	Ser-736 to Gly-741,
	1001	989																					
	1 - 429	138 - 3230																					
	403	88																					
	781600	1225632								_													
		HELHB88																					
		78																					

D9764875 D11791

	AR061: 5, AR089: 1 H0616: 1 and L0758: 1.	AR061: 24, AR089: 14 L0806: 3, L0772: 2, L0648: 2, H0255: 1, L0717: 1, H0586: 1, H0599: 1, H0618: 1, H0581: 1, H0052: 1, H0123: 1, L0629: 1, L0659: 1, L0663: 1, S0330: 1, H0518: 1 and H0555: 1.	AR089: 0, AR061: 0 S0354: 1, L0657: 1, H0144: 1 and S0330: 1.
Phe-762 to Asp-768, Glu-808 to Val-815, Ser-847 to Trp-856, Asp-858 to Trp-876, Gln-892 to Ala-898, Pro-964 to Ile-976. Arg-1 to His-10.	Ile-33 to Ser-40, Val-63 to Gln-69, Phe-84 to Ser-94, Lys-205 to Lys-212. Ser-38 to Pro-45	Gly-5 to Gln-15, Gly-104 to Gly-111, Gly-136 to Asp-141, His-228 to Pro-234. Gln-39 to Thr-51, Lys-93 to Ala-106, Gln-112 to Pro-129, Pro-132 to Pro-143.	Ser-119 to Thr-127, Gln-134 to Ser-152.
1002	687	688	689
136 - 567	1 - 669	704 - 3	3 - 674
404	89	90 406	91
811935	1152261	813296	815845
	HTEMV66	HMTAJ73	НЕ9ТD31
	79	08	81

AR089: 1, AR061: 1 S0040: 1, H0014: 1, H0030: 1, H0063: 1, L0803: 1, H0521: 1 and S0028: 1.		AR061: 6, AR089: 2 L0758: 6, L0794: 3,	H0038: 2, L0768: 2,	L0790: 2, L0731: 2,	S0342: 1, H0664: 1,	H0616: 1, S0210: 1,	L0773: 1 and L0608: 1.		AR061: 1, AR089: 0 H0457: 2, H0650: 1 and H0622: 1.		AR089: 6, AR061: 2 H0013: 2, H0046: 2, H0036: 1 H0500: 1	H0581: 1, H0551: 1 and H0494: 1.
Gly-1 to Ala-8, Phe-31 to Leu-36, Glu-54 to Lys-62, Gly-69 to Gly-75, Leu-100 to Gly-106, Ser-125 to Lys-131. Gly-1 to Ala-8,	Phe-31 to Leu-36, Glu-54 to Lys-62, Gly-69 to Gly-75, Leu-100 to Gly-106.	Ala-12 to Trp-19, Ala-21 to Arg-27,		~ £		Tyr-164 to Ala-169.			Asp-27 to Val-32, Asp-66 to Gly-71.	Arg-8 to Arg-17, Asp-47 to Val-52, Asp-86 to Gly-91.		
690		691						1006	692	1007	693	
26 - 535		2 - 508						3 - 527	1 - 972	2 - 448	1 - 732	
92		93						408	94	409	95	
1141363		1125914						815891	1020119	827630	1165423	
HGBDG55 1141363		НООНГЗ							HEOPP67		HKAOV71	
82		83							84		85	

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	AR089: 7, AR061: 3	L0766: 14, H0521: 4,	L0/48: 4, L0804: 3,	L0776: 3, L0749: 3,	L0731: 3, L0485: 3,	S0376: 2, H0580: 2,	L0483: 2, H0316: 2,	S0002: 2, L0803: 2,	L0775: 2, L0805: 2,	L0659: 2, L0438: 2,	H0265: 1, H0686: 1,	H0656: 1, H0341: 1,	S0212: 1, H0638: 1,	H0125: 1, S0360: 1,	H0411: 1, S0222: 1,	H0409: 1, H0587: 1,	H0014: 1, S0003: 1,	H0163: 1, H0591: 1,	H0488: 1, H0494: 1,	H0641: 1, L0598: 1,	H0529: 1, L0772: 1,	L0764: 1, L0768: 1,	L0774: 1, L0655: 1,	L0783: 1, L0809: 1,	L0792: 1, L0663: 1,	L0665: 1, H0702: 1,	H0519: 1, S0126: 1,	H0682: 1, H0435: 1,	H0672: 1, H0704: 1,
	Leu-12 to Gln-21.																												
1008	694		_																										
1 - 732	2 - 361																												
410	96																												
827679	1137752																												
	нрош90																												
	98					•																							

S3012: 1, L0751: 1, L0750: 1, L0777: 1, L0752: 1, L0757: 1, L0758: 1, L0759: 1, L0362: 1, H0423: 1 and H0506: 1.	-	AR050: 10, AR051: 3 AR061: 1, AR089: 1, AR054: 0	S0028: 4, S0001: 2, S0278: 2, S0050: 2,	S0282: 1, H0632: 1,	H0027: 1, S0038: 1,	S0052: 1, S0053: 1, H0684: 1 and S0044: 1.					AR089: 1, AR061: 0	H0620: 2, H0012: 1, S0152: 1 and S0260: 1.		AR061: 402, AR089:	142	H0038: 7, L0758: 5, H0616: 4, L0731: 4,
					٠		Gly-113 to Gly-119,	Gln-173 to Thr-181, Ala-362 to Pro-368.		Leu-51 to Ser-62.				Ser-83 to Lys-88,	Pro-95 to Asn-112,	Arg-180 to Asp-185, Met-231 to Arg-240.
	1009	969					1010	,	1011	1012	969		1013	269		
	221 - 724	2331 - 598					1 - 1116		1 - 435	138 - 587	487 - 8		3 - 440	2590 - 1844		
	411	26					412		413	414	86		415	66		
	831976	1182552			-		833061		973206	973208			836491	1219300		
		HFRBN81				-					HFKJW01			HSDFL63		
		87									88			68		

S0002: 3, L0637: 3, H0623: 2, L0794: 2, L0809: 2, L0663: 2, H0522: 2, L0779: 2, L0777: 2, S0046: 1, H0431: 1, T0060: 1, H06431: 1, S0010: 1, H01328: 1, H0135: 1, H0163: 1, H0412: 1, H0163: 1, H0412: 1, H0163: 1, L0768: 1, L0803: 1, L0375: 1, L0803: 1, L0375: 1, L0864: 1, L0647: 1, L0664: 1, H0693: 1, S0328: 1, S0168: 1,		AR061: 0, AR089: 0 S0152: 2	AR061: 4, AR089: 3 H0038: 7, L0758: 5, H0616: 4, L0731: 4, S0002: 3, L0637: 3, H0623: 2, L0794: 2,
	Glu-1 to Asp-7, Met-53 to Met-60, Ile-78 to Ser-83.	His-8 to Gly-18, Leu-40 to Ile-45, Asn-100 to Asp-105.	Glu-4 to Ser-9, Ser-58 to Arg-65.
	1014	869	669
	1 - 249	39 - 377	1 - 714
	416	100	101
	836498	836503	836514
		HPJET90	HEMFC61
		06	91

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	4		2					
L0809: 2, L0663: 2, H0522: 2, L0779: 2, L0777: 2, S0046: 1, H0431: 1, T0060: 1, H0013: 1, S0010: 1, H0545: 1, H0050: 1, S0023: 1, S0003: 1, H0163: 1, H01135: 1, H0163: 1, H0412: 1, L0102: 1, L0768: 1, L0803: 1, L0768: 1, L0542: 1, L0647: 1, L0542: 1, L0791: 1, L0567: 1, L0791: 1, L0664: 1, H0693: 1, S0328: 1, S0168: 1,	AR089: 41, AR061: H0486: 2		AR061: 4, AR089: 2 L0754: 6, L0766: 3.	L0731: 2, H0624: 1, H0170: 1, S0116: 1	S0280: 1, H0545: 1,	T0006: 1, S0344: 1,	30420: 1, L0//0: 1, r 0700: 1 r 0748: 1	L0/90: 1, L0/46: 1, L0756: 1, L0779: 1,
	Thr-26 to Arg-31, Gly-73 to Trp-78.	Ala-2 to Glu-7, Arg-50 to Glu-58.	Gly-1 to Ser-6, Arg-76 to Gln-88.				Ser-294 to 1nr-299.	
	700	1015	701					
	467 - 234	130 - 342	1 - 897					
	102	417	103					
	1174351	846630	847143					
	HDTBR50		НАССН94					
	92		93					

L0589: 1 and L0462: 1.	AR061: 2, AR089: 2 L0438: 4, L0746: 4,	H0581: 2, H0656: 1, H0013: 1, L0471: 1,	H0266: 1, H0328: 1, H0553: 1, S0438: 1,	H0529: 1, L0766: 1,	E0003: 1, F0320: 1, H0521: 1, L0752: 1 and S0192: 1.			AR061: 6, AR089: 3 H0550: 1, H0494: 1	and L0659: 1.		AR061: 1, AR089: 1 H0305: 1 and H0589:	- 1	AR061: 5, AR089: 2 H0650: 2 H0052: 2	H0547: 2, H0542: 2,	S0212: 1, S0222: 1,	T0114: 1, L0483: 1,	H0628: 1, L0455: 1,	H0413: 1, S0344: 1,	L0/66: 1, L0/75: 1, L0805: 1, L0665: 1,
	Thr-21 to Trp-26, Thr-72 to Val-88,	Arg-115 to Tyr-127.				Ser-8 to Thr-15,	Arg-73 to Thr-79, Phe-86 to Leu-92.			Arg-1 to Thr-14.			Gln-57 to Ile-67,	Asp-// to Asp-o5.					
	702					1016		703		1017	704		705					<u> </u>	
	441 - 1166					3 - 470		525 - 1		2 - 397	3 - 311		3 - 470						
	104					418		105		419	106		107						
	1223481		,			849161		1140393		851207			853149						
	HE8TI39							HEGAP32			HCWFU66		HUSYI29						
	94							95			96		62		<u> </u>			_	

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H0520: 1, H0519: 1, S0126: 1, H0521: 1, S0044: 1, S0390: 1, L0592: 1 and S0026: 1.	AR061: 1, AR089: 1 H0175: 1, H0266: 1, H0292: 1, H0628: 1 and L0779: 1.		AR061: 1, AR089: 0 H0494: 2, H0693: 2, H0521: 2, H0580: 1,	H0253: 1, H0628: 1, H0522: 1 and H0422: 1.			AR089: 1, AR061: 1	S0198: 57, S0274: 12, S0252: 4, S0270: 3,	S0264: 1, S0268: 1 and	S0228: 1.		AR050: 16, AR054: 10, AR051: 5, AR061:	2, AR089: 1	H0305: 4, S0282: 1,	H0575: 1, H0150: 1 and H0617: 1.	
	Gly-61 to Glu-67, Ala-88 to Gly-96, Gly-127 to Trp-137.		Gln-1 to Gln-6, Ser-24 to Thr-31, Pro-57 to Gln-63,	Ala-96 to Met-104, Asn-124 to Lys-133.	Ser-172 to Trp-182,	Ser-186 to Glu-194, Pro-286 to Pro-294.	Gln-154 to Ser-163.				Gln-154 to Ser-163.	Ser-59 to Ile-66, Arg-73 to Gly-85.				
	706	1018	707				708				1019	402				1020
	82 - 933	2 - 349	54 - 977				3 - 704				3 - 704	827 - 1222				3 - 359
	108	420	109				110				421	111				422
	1134131	856149	863023				865922		-		908115	637493				872075
	HMEFT66		HKAAR71				H7TBC95					HAPPX52				
	86		66				100				_	101				

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	AR089: 1, AR061: 0 H0617: 2, H0013: 1,	H02/1: 1, L0455: 1 and H0539: 1.					AR089: 1, AR061: 1 H0620: 2	AR089: 4, AR061: 3	T0010: 3, S0049: 2,	H0052: 2, L0415: 1, H0618: 1 and S0010: 1.		AR054: 29, AR051: 12, AR061: 6, AR089:	3, AR050: 2 H0196: 1 and H0266: 1.		AR061: 2, AR089: 1	H0013: 1 and S0126: 1.	
His-73 to Phe-81, Thr-92 to Trp-102.	Lys-1 to Lys-6, Gln-25 to Asp-36,	Ser-85 to 116-96, Val-115 to Ser-136,	Lys-172 to Trp-177,	Pro-188 to Phe-201,	Asn-230 to Gly-239.			Gly-2 to Thr-10,	Glu-160 to Gly-175,	Thr-189 to Glu-197.	Gly-2 to Thr-10, Glu-99 to Gly-104.	Asp-13 to Asp-19, Lys-76 to Asp-84.		Asp-13 to Asp-19,	Asp-28 to Ser-36,	Glu-47 to Gln-60,	Phe-68 to Gly-77, Pro-81 to Val-86.
1021	710					1022	711	712			1023	713		1024	714		
400 - 2	1 - 756					1 - 684	3 - 308	196 - 786			189 - 662	2 - 547		1 - 315	2 - 277		
423	112					424	113	114			425	115		426	116		
872076	1152326					878322	880220	1165362			880297	1092158		887791	1129488		
	HBGSJ13						HFKLX38	HTLGP15				HMEGH46			HE8PY29		
	102						103	104				105			106		

	125264, 134570, 600511, 601556
	6p24-p23
	AR089: 1, AR061: 0 L0747: 28, L0588: 22, L0757: 19, H0251: 15, S0358: 14, S0045: 13, L0731: 12, H0551: 10, H0412: 10, L0771: 10, L0748: 9, L0778: 9, H0506: 9, H0556: 8, S0046: 8, H0622: 8, H0013: 7, H0623: 7, L0662: 7, S0192: 7, S0003: 6, L0599: 6, L0439: 6, L0750: 6, L0439: 6, L0750: 6, L0759: 6, L0750: 6, L0759: 6, L0599: 6, L0768: 6, S0040: 5, S0360: 5, H0581: 5, H0144: 5, S0026: 5, S0312: 4, H0486: 4, H0674: 4, L0776: 4, S0126: 4, H0672: 4, S0136: 4, L0752: 4, H0624: 3, S0420: 3, H0624: 3, S0420: 3,
Asp-28 to Ser-36, Glu-47 to Gln-60, Phe-68 to Gly-77, Pro-81 to Val-86.	Asp-1 to Gly-14, Ala-60 to Lys-71, Gln-101 to Glu-118.
1025	715
2 - 277	3 - 605
427	117
887862	890384
	HTDAB17
	107

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H0266: 3, H0615: 3,	H0031: 3, H0553: 3,	91: 3, H0264: 3,	H0413: 3, H0494: 3,	S0210: 3, L0770: 3,	50806: 3, H0519: 3,	H0435: 3, L0740: 3,	.0751: 3, L0749: 3,	H0170: 2, H0657: 2,	H0656: 2, S0356: 2,	S0408: 2, H0619: 2,	93: 2, H0333: 2,	40: 2, H0427: 2,	S0280: 2, H0156: 2,	18: 2, H0596: 2,	T0110: 2, H0545: 2,	46: 2, H0009: 2,	H0050: 2, L0471: 2,	H0188: 2, H0328: 2,	H0428: 2, L0483: 2,	H0644: 2, H0038: 2,	S0426: 2, L0772: 2,		C0649: 2, L0651: 2,	.0655: 2, L0789: 2,	.0663: 2, L0665: 2,	L0352: 2, H0658: 2,	52: 2, H0521: 2,	H0696: 2, S0404: 2,	H0555: 2, S0028: 2,	H0445: 2, L0591: 2,
H026	:00H	H059	H04	S021)80T	H04.	L075	H01,	H06	S04(H03	700 <u>L</u>	S028	H03	T01	00H	H00	H01	H04	90H	S04,	7007	90T	106	T06	103	S01:	90H	H05	H04
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)543: 2,	5024: 1,	0049: 1,)661: 1,	0664: 1,	0005: 1,	376: 1,	0351: 1,	0431: 1,	1, H0403: 1,	1, H0587: 1,	H0574: 1,	, L0021: 1,	1, H0274: 1,	0048: 1,	H0434: 1,	, H0196: 1,	0263: 1,	0572: 1,	0620: 1,	0024: 1,	1, H0051: 1,	[0510: 1,	, H0288: 1,	H0039: 1,	10628: 1,	[0212: 1,	[0163: 1,	[0040: 1,	[0087: 1,
L0594: 2, H0543: 2	H0265: 1, St	H0295: 1, T0049: 1	S0134: 1, H(H0663: 1, H0664:	S0418: 1, L0005: 1,	S0354: 1, S0	S0468: 1, H	S0220: 1, H	H0392: 1, H	H0592: 1, H		์ —ี่	H0575: 1, H		·	H0230: 1, H	H0052: 1, H	H0597: 1, H	H0012: 1, H0620: 1	T0003: 1, H0024:	H0057: 1, H	H0083: 1, H	H0687: 1, E	S0022: 1, H	` ←	H0166: 1, H0212:	H0135: 1, F	H0090: 1, H0040: 1,	H0634: 1, H0087:
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H0477: 1, H0488: 1, H0433: 1 H0268: 1	H0269: 1, H0056: 1,	S0038: 1, H0100: 1,	H0429: 1, S0450: 1,	H0132: 1, H0633: 1,	S0472: 1, H0647: 1,	H0646: 1, H0652: 1,	S0344: 1, L0640: 1,	L0371: 1, L0372: 1,	L0374: 1, L0767: 1,	L0768: 1, L0364: 1,	L0794: 1, L0650: 1,	L0375: 1, L0378: 1,	 L0783: 1, L0647: 1,	S0374: 1, T0068: 1,	L0438: 1, H0547: 1,	H0689: 1, H0711: 1,	H0684: 1, H0659: 1,	H0670: 1, H0648: 1,	S0330: 1, S0378: 1,	S0380: 1, H0709: 1,	S0146: 1, S3012: 1,	S0037: 1, S0206: 1,	۲,	`	S0434: 1, S0436: 1,	L0584: 1, L0593: 1,	L0362: 1, S0011: 1,	S0424: 1 and H0293: 1.
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AR089: 14, AR061: 7	H0341: 1 and H0422:					AR061: 3, AR089: 3	L0759: 12, L0439: 11,	L0766: 7, L0775: 5,	H0521: 5, L0755: 5,	L0748: 4, L0756: 4,	L0777: 4, L0731: 4,	L0581: 4, L0619: 3,	L0666: 3, L0779: 3,	L0757: 3, L0588: 3,	S0418: 2, L0618: 2,	H0580: 2, L0055: 2,	L0769: 2, L0773: 2,	L0774: 2, L0791: 2,	L0747: 2, L0750: 2,	H0265: 1, H0663: 1,	S0356: 1, H0208: 1,	H0370: 1, H0108: 1,	H0575: 1, H0618: 1,	H0544: 1, H0545: 1,	S0050: 1, H0510: 1,	H0286: 1, H0031: 1,	H0644: 1, H0068: 1,	H0135: 1, L0564: 1,	H0494: 1, L0475: 1,
	Gln-49 to Ala-58,	Gly-175 to Gly-182,	Arg-184 to Leu-191,	Pro-198 to Phe-205.	Arg-1 to Glu-8.	Arg-1 to Thr-7,	Pro-19 to Ala-25,	Pro-56 to Leu-64,	His-72 to Asn-81,	Phe-184 to Pro-192,	Pro-218 to Val-226,	Ser-229 to Arg-236.)																
716					1026	717																							
1 - 780					2 - 298	2 - 709																							
118					428	119																							
1199931					894415	1194798																							
HCFCF47 1199931						HDOHB19																							
108						109																							

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H0396: 1, S0144: 1, S0002: 1, S0426: 1, L0763: 1, L0761: 1, L0642: 1, L0764: 1, L0662: 1, L0768: 1, L0806: 1, L0661: 1, L0659: 1, L0367: 1, L0663: 1, H0519: 1, H0435: 1, L0751: 1, L0749: 1, L0603: 1, H0665: 1 and H0542: 1.	•			AR050: 17, AR051:	11, AK054: 2, AK089:	1, AR061: 0	S0010: 1 and S0027: 1						AR061: 1, AR089: 1	H0575: 2, L0754: 2,	H0599: 1, T0048: 1,	L0163: 1, H0051: 1, H0188: 1, H0379: 1,
	Pro-14 to Ala-20,	Pro-51 to Leu-59,	C1 52 T 20	Gln-22 to Lys-30,	Phe-40 to 1 yr-49,	Gln-70 to Trp-75,	Arg-80 to Gln-87,	Gly-95 to Arg-101.	Pro-9 to Gln-16,	Phe-31 to Tyr-40,	Gln-61 to Trp-66,	Arg-71 to Gln-78,	Gln-43 to Thr-58,	Asn-74 to His-79,	Gly-109 to Trp-114,	Asp-136 to Phe-145.
	1027		- }	718					1028				719			
	2 - 538			3 - 329	-				129 - 428				2 - 562			
	429			120					430				121			
·	895106			1129154					895963				1162672			
				HAGDN53									HUFDB74			
			;	110									1111			

																					
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L0438: 1, H0670: 1, H0672: 1, L0439: 1, L0747: 1, S0260: 1, L0591: 1 and H0506:		AR054: 20, AR050: 15, AR061: 7, AR089:	4, AR051: 1 S0053: 1			AR061: 6, AR089:	H0617: 10, L0665: 4,	H0333: 3, S0366: 3,	L0759: 3, H0599: 2,	L0648: 2, L0653: 2,	L0664: 2, H0519: 2,	H0686: 1, H0484: 1	H0664: 1, H0392: 1	L0622: 1, S0280: 1,	H0545: 1, T0010: 1	H0424: 1, H0031: 1	H0181: 1, H0708: 1	H0494: 1, H0633: 1	L0371: 1, L0764: 1,	L0773: 1, L0768: 1,	L0375: 1, L0651: 1,
	Gln-43 to Thr-58, Asn-74 to His-79, Gly-109 to Trp-114.	His-8 to Gly-18, Ala-39 to Gly-45,	~ Ci	His-8 to Gly-18,	Ala-39 to Gly-45, Pro-94 to Glu-101.	Glu-1 to Ala-12,	Glu-19 to Val-28,	Glu-34 to Thr-45,	Leu-140 to Asp-157,		Ala-211 to Asp-216.										
	1029	720		1030		721						-									
	2 - 412	28 - 516		28 - 480		11 - 790															
	431	122		432		123															
	901451	1092567	-	903741		1188175	**														
		HNHFH24				HBGQT03	,														
		112				113															

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L0659: 1, L0783: 1, L0789: 1, L0438: 1, H0684: 1, H0670: 1, L074: 1, L0780: 1, L075: 1 and L0595: 1.	,			AR061: 4, AR089: 2 H0046: 1 and I 0758:	1.	•	AR061: 6, AR089: 5	L0770: 4, L0789: 3,	L0439: 3, L0750: 3,	L0641: 2, L0747: 2,	L0758: 2, S0040: 1,	H0575: 1, T0010: 1,	H0087: 1, S0422: 1,	L0803: 1, L0375: 1,	L0776: 1, L0659: 1,	L0783: 1, H0144: 1,	L0352: 1, H0684: 1,	H0660: 1, S0027: 1,	L0777: 1 and H0445: 1.		
	Lys-1 to Ala-15, Glu-22 to Val-31,	Glu-37 to Thr-48, Leu-143 to Asp-160, Thr-170 to Ala-201,	Ala-214 to Asp-219.	Asp-119 to Tyr-124.			Arg-9 to Gln-17,	Ile-33 to Asn-39,	Gln-93 to Ser-104,	Asp-141 to Leu-155,	Ser-224 to Asn-234,	Asn-243 to Lys-248,	Ser-308 to Gln-320,	Thr-350 to Glu-357,	Ser-384 to Thr-390,	Asp-435 to Ser-447,	Ala-480 to Lys-487,	Lys-496 to Leu-508,	Ser-519 to Val-528,	Ser-533 to Gln-541.	Arg-9 to Leu-15.
	1031			722		1032	723														1033
	3 - 791			3 - 482		3-416	199 - 1821														199 - 909
	433			124		434	125														435
	908173			1103959		909762	1204931		_												762606
				HETLF29			HOUGD29														
				114			115														

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13		1					 ,		4	.				
AR089: 13, AR061: 13 L0666: 3, L0758: 3, H0616: 2, L0779: 2, S0036: 1, L0598: 1, L0766: 1, L0651: 1, L0806: 1, L0776: 1, H0144: 1, H0547: 1, H0672: 1 and H0555: 1.		AR089: 1, AR061: S0007: 1, S0222: 1	S0049: 1, L0438: 1,	110020. 1 alla 20407.					AR061: 9, AR089: H0624: 1			AR061: 2, AR089:	H0229: 1, H0590: 1,	S0049: 1, H0014: 1, H0560: 1, L0439: 1 and
Asp-22 to Asp-28, Leu-98 to Trp-103, Glu-123 to Trp-154, Pro-158 to Gln-178, Pro-180 to Met-189, Glu-207 to Lys-226, Ser-231 to Leu-237.	Asp-22 to Asp-28, Leu-98 to Trp-103, Glu-123 to Trp-154.	Phe-2 to Gln-9,	Glu-51 to Leu-64,	Glu-98 to Thr-104,	Ala-119 to Asp-126,	A1 2 C1 0	Ala-2 to Gin-9,	Arg-22 to Val-29, Glu-51 to Leu-64.		Leu-10 to Gly-16,	Glu-78 to Cys-87.	Val-10 to Gly-16,	Met-19 to Val-34,	Ala-84 to Asp-90, Met-107 to Trp-120,
724	1034	725				0.00	1035		726	1036		727		
1 - 711	1 - 711	3 - 614					7 - 658		708 - 166	2 - 796		3 - 974		
126	436	127				100	437		128	438		129		
1128254	909843	1128964				0,000	909942		1149808	909948		1105444		
HTEMV09 1128254		HNTNB14							HE2KZ07			HSIGN57		
116		117							118			119		

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H0543: 1.				AR061: 8, AR089: 5	L0456: 3, H0024: 2	and L0747: 1.					S0007: 2, L0794: 2,	S0434: 2, S0354: 1,	N0006: 1, H0622: 1 and	H0478: 1.			~		AR061: 2, AR089: 2	L0439: 6, L0777: 6,	H0052: 4, L0748: 4,	H0634: 3, L0662: 3,	L0805: 3, L0659: 3,	L0438: 3, H0547: 3,	L0750: 3, L0758: 3,	H0208: 2, H0123: 2,	H0014: 2, H0617: 2,	H0135: 2, L0769: 2,
Gln-191 to Ala-201,	Glu-223 to Val-229, Asn-309 to Gly-314.	Val-10 to Gly-16,	Met-19 to Val-34.	Gln-7 to Glu-17,	Thr-36 to Asn-42,	Val-44 to Phe-49,	Tyr-76 to Ile-85,	Cys-94 to Glu-99,	Pro-105 to Ser-110.	Gln-7 to Glu-17.	Ser-45 to Glu-53,	Ile-78 to Asn-94,	Leu-99 to Ser-104,	Ser-110 to Trp-128,	Tyr-145 to Gly-153,	Gln-168 to Trp-173,	Leu-196 to Ala-205.	Ser-6 to Trp-24.	Glu-29 to Arg-35,	Arg-50 to Leu-55,	Leu-60 to Ser-69,	Lys-102 to Asp-108,	Pro-227 to Glu-233,	Leu-249 to Glu-261.				
		1037		728						1038	729							1039	730									
		2 - 760		39 - 512						39 - 512	172 - 1368							3 - 410	786 - 1628									
		439		130						440	131							441	132									
		910078		1106654			-, ·			910079	1195217							911264	1217208									
				HLHBC30						-	HFBDJ13								HTPGG25									
				120							121								122									

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L0766: 2, L0803: 2, L0776: 2, L0666: 2,	L0751: 2, L0745: 2, L0731: 2, H0265: 1,	S0408: 1, H0549: 1,	H0497: 1, L0622: 1,	H0581: 1, H0194: 1,	L0738: 1, H0546: 1,	H0024: 1, S0362: 1,	L0163: 1, T0010: 1,	H0083: 1, H0510: 1,	H0266: 1, H0428: 1,	H0622: 1, H0673: 1,	H0598: 1, S0036: 1,	H0163: 1, H0413: 1,	L0370: 1, T0041: 1,	H0647: 1, L0637: 1,	L0667: 1, L0772: 1,	L0646: 1, L0800: 1,	L0764: 1, L0649: 1,	L0657: 1, L0809: 1,	L0788: 1, L0663: 1,	S0374: 1, H0520: 1,	H0670: 1, H0666: 1,	S0330: 1, H0539: 1,	H0521: 1, H0696: 1,	H0478: 1, S0028: 1,	L0741: 1, L0747: 1,	L0749: 1, L0780: 1,	L0752: 1 and H0543: 1.
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	4, AR089:	L0439: 6, L0777: 6, H0052: 4, L0748: 4,	.0662:	L0805: 3, L0659: 3,	.0438: 3, H0547: 3	.0750: 3, L0758: 3	H0123:	10617:	H0135: 2, L0769:	.0803:	.0666:	L0751: 2, L0745: 2,	2, H0265:	1, H0549:	H0497: 1, L0622:	1, H0194:	, H0546:	, S0362:	T0010:	H0510:	l, H0428:	1, H0673:	1, S0036:	H0163: 1, H0413:	.0370: 1, T0041:	L0637:	L0667: 1, L0772:	.0800
	51: 4,	39: 0, 32: 4, L	34: 3, L	5:3, T	8: 3, H	0:3,L	H0208: 2, H0123:	H0014: 2, H0617	35: 2, I	56: 2, L	76: 2, L	51: 2, L	31: 2, F	8: 1, E	97: 1, I	81: 1, I				H0083: 1, I	H0266: 1, I	H0622: 1, I	H0598: 1, 9	63: 1, 1	70: 1, 7	H0647: 1,]	67: 1, I	1.0646: 1, 1.0800:
	AR061:	H005	H063	L080	L043	L075	H02(H00	H01.	L076	L077	L075	L0731: 2	S0408: 1	H04	H0581:	L0738:	H0024:	L0163: 1	00H	H02	90H	H05	H01	L03,	90H	90T	1,06
	-35,	69.	p-108,	1-141.																								
Arg-8	to Arg	to Leu to Ser-	2 to As	3 to Glr																								
Pro-3 to Arg-8.	Glu-29 to Arg-35,	Arg-50 to Leu-55, Leu-60 to Ser-69.	Lys-102 to Asp-108	Pro-133 to Gln-141.																								
1040	731			<u>- </u>							-		**															
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3 - 392	56 - 553																											
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L0764: 1, L0649: 1, L0657: 1, L0809: 1, L0788: 1, L0663: 1, S0374: 1, H0520: 1, H0670: 1, H0666: 1, S0330: 1, H0539: 1, H0521: 1, H0696: 1, H0478: 1, S0028: 1, L0741: 1, L0747: 1, L0749: 1, L0780: 1,	AR089: 1, AR061: 1 S0354: 16, H0457: 7, L0758: 3, H0555: 2, H0170: 1, H0662: 1, S0360: 1, H0036: 1, H0150: 1, H0051: 1, H0553: 1, L0800: 1, L0644: 1, L0771: 1, L0663: 1, H0144: 1, S0374: 1, H0670: 1, H0522: 1, L0749: 1,	
	Ser-15 to Leu-21, Pro-24 to Val-30, Ser-91 to Lys-99, Thr-113 to Lys-120, Pro-168 to Gln-174, Glu-226 to Ser-231, Ser-296 to Gln-307, Asp-319 to Gly-328, Gly-330 to Ala-337.	Ser-11 to Leu-17, Pro-20 to Val-26, Ser-87 to Lys-95, Thr-109 to Lys-116, Pro-164 to Gln-170,
	732	1041
	2 - 1012	2 - 1000
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	124	

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	H0052: 1 and L0471:	AR089: 0, AR061: 0 H0583: 1, H0644: 1, L0766: 1 and H0518: 1.		AR089: 2, AR061: 2	L0766: 5, L0776: 5,	L0754: 4, H0013: 3,	S0126: 3, L0742: 3,	,0750: 3, H0624: 2,	,0360: 2, H0560: 2,	.0769: 2, L0641: 2,	L0665: 2, S0330: 2,	.0756: 2, L0731: 2,	.0759: 2, L0588: 2,	H0171: 1, H0650: 1,	H0402: 1, H0638: 1,	10340: 1, H0637: 1,	10351: 1, S0222: 1,	H0581: 1, H0263: 1,	H0545: 1, H0050: 1,	S0051: 1, S0214: 1,	H0039: 1, L0055: 1,	H0090: 1, H0412: 1,
7, 33, 33,]	A J		A			<u>\(\text{\cdot} \) \(\text{\cdot} \)</u>		•					<u> 14</u>	نبز	<u>ن</u> ــــــــــــــــــــــــــــــــــــ	_ <u>i</u>	<u>;+;</u>	<u>- <u>- 1</u></u>	<u>0</u>	<u> </u>	<u>بطر</u>
Glu-222 to Ser-227, Ser-292 to Gln-303, Asp-315 to Gly-324, Gly-326 to Ala-333.	Thr-2 to Gln-7.	Ile-26 to Trp-33, Glu-52 to Leu-71.	Ile-26 to Trp-33, Glu-52 to Leu-71.	Pro-1 to Glu-15,	Ala-26 to Lys-32,	Glu-46 to Leu-65,	Arg-82 to Cys-94,	Leu-101 to Glu-107,	Leu-146 to Asp-151,	Gln-157 to Ser-162,	Ser-165 to Ala-187,	Phe-210 to Leu-217.										
	733	734	1042	735																		
	3 - 314	1 - 363	1 - 363	1 - 657																		
	135	136	444	137																		
	911374	1071602	911385	1194697	_						-											
	HCEPW85	HMTAW83		HDMAV01																	_	
	125	126		127																		

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H0022: 1, H0359: 1, H0561: 1, H0641: 1, L0770: 1, L0637: 1, L0646: 1, L0764: 1, L0773: 1, L0662: 1, L0773: 1, L0659: 1, L0653: 1, L0659: 1, L0792: 1, H0519: 1, H0522: 1, H0576: 1, S0028: 1, L0439: 1, L0770: 1, H0444: 1, L0777: 1, H0444: 1, L0596: 1, L0601: 1,		AR050: 48, AR054: 42, AR051: 35, AR089: 3, AR061: 1 H0575: 2, H0580: 1, S0002: 1, S0426: 1, H0521: 1, H0436: 1 and	AR089: 8, AR061: 3 L0794: 3, L0758: 2, L0759: 2, H0624: 1, L0717: 1, T0082: 1,
	Asp-1 to Glu-11, Ala-22 to Lys-28, Glu-42 to Leu-61, Arg-78 to Cys-90,	7. 4.	Pro-4 to His-21, Glu-35 to Gln-43.
	1043	736	737
	3 - 428	212 - 583	1212 - 937
	445	138	139
	911386	911396	1160657
		HDPSR74	HHEZT58
		128	129

		109400, 132800, 132800.	186855, 223900,	253800,	253800,	602088													
		9q31																	
H0581: 1, H0553: 1, H0038: 1, T0067: 1, L0665: 1, H0436: 1, L0439: 1, L0745: 1 and H0543: 1.		AR061: 8, AR089: 7 H0253: 3, H0618: 1 and L0758: 1.					AR061: 6, AR089: 5	H0253: 18, H0618: 7,	L0794: 3, H0038: 1,	H0616: 1, L0788: 1 and	L0758: 1.								AR061: 373, AR089: 188
	Glu-9 to Lys-14, Gln-51 to Gln-57.	Pro-89 to Ala-97.						Pro-118 to Lys-128,			Ser-322 to Gly-344,	Pro-347 to Ser-353.	Ser-54 to Lys-61,	Pro-118 to Lys-128,	Thr-208 to Ser-213,	Ser-218 to Ala-227,	Pro-230 to Ser-236,	Pro-238 to Ser-244.	-
	1044	738					739						1045						740
	1 - 558	2 - 469					144 - 1211						92 - 856						38 - 1096
	446	140	-				141						447						142
	911416	911649					1189721						911654						911655
		HTLDU05					HTLET56												HTLCA95
		130					131												132

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H0253: 3, H0618: 2, H0038: 2, H0616: 1 and L0758: 1.	AR089: 1, AR061: 1 L0794: 3, H0038: 2,	H0265: 1, S0358: 1, T0039: 1, H0616: 1,	L0768: 1, L0804: 1,	L0664: 1, L0777: 1, L0731: 1, L0758: 1 and L0465: 1.				AR089: 19, AR061: 13 H0618: 14. H0253: 12.	H0038: 11, H0616: 2,	L0794: 1, L0779: 1 and	L0758: 1.					AR089: 18, AR061: 5 H0618: 5, H0549: 1	and H0543: 1.		AR061: 1, AR089: 0	20040: 1 and 302/8: 1.	AR089: 1, AR061: 1
	Ala-39 to Ala-45, Gln-57 to Ser-63,				Ala-39 to Ala-45,	Gln-57 to Ser-63,	Tyr-90 to Lys-95.	Gly-23 to Asn-30, Thr-58 to Val-79.	Arg-101 to Ile-106,	Thr-117 to Glu-126,	Pro-184 to Lys-193,	Ile-298 to Val-303,	Phe-381 to Leu-389.	Gly-23 to Asn-30,	Arg-45 to Lys-50.	Gly-35 to Ser-44.		Val-6 to Arg-12.	Pro-89 to Leu-102.	20 10 171	Asp-16 to Gln-22,
	741				1046			742					•	1047		743		1048	744	1	745
	1 - 1119				1 - 411			22 - 1359	•					22 - 1167		216 - 587		93 - 464	3 - 317		507 - 1
	143				448			144						449		145		450	146	,	147
	1090517				911656			1134919		-				911666		1135518		915136	918119		982250
	HTEJT86				1			HTEMA54								HTLGJ17			HOUES64		HMSCD15
	133							134								135			136		137

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S0002: 2 and L0766: 1.		AR089: 30, AR061: 4	H0521: 3, H0051: 2,	L0756: 2, H0590: 1,	S0250: 1, L0772: 1,	H0522: 1, S0406: 1 and	L0748: 1.								AR089: 1, AR061: 1	L0439: 3, L0438: 2,	S0028: 2, H0656: 1,	H0645: 1, H0369: 1,	S0222: 1, S0346: 1,	H0328: 1, H0029: 1,	H0644: 1, H0169: 1,	H0591: 1, H0646: 1,	H0520: 1, H0539: 1,	L0746: 1 and L0366: 1.		AR061: 5, AR089: 2	L0770: 4, L0803: 4,	H0638: 1, H0123: 1,	S0426: 1, L0662: 1,
Val-44 to Ser-57.		Met-7 to Ser-12,	Ser-20 to Arg-30,	Asp-85 to Ala-92,	Met-119 to Asn-146,	Pro-151 to Asp-161,	Gln-253 to Glu-260,	Ile-333 to Val-342,	Leu-396 to Ala-406.	Met-7 to Ser-12,	Ser-20 to Arg-30,	Asp-85 to Ala-92,	Met-119 to Asn-146,	Pro-151 to Asp-161.	His-35 to Glu-44,	Lys-88 to Tyr-94,	Asp-140 to Ser-152,	Leu-166 to Lys-171,	Glu-183 to Glu-197,	Glu-210 to Leu-217,	Pro-231 to Gln-236.					Ser-1 to Gly-12,	Arg-30 to Pro-36,	Thr-65 to Met-76,	Pro-86 to Asp-95.
	1049	746								1050					747										1051	748			·
	237 - 635	228 - 1715								210 - 1037					3 - 1352										3 - 1310	1146 - 832			
	451	148			-					452					149										453	150			
	918133	1223474								919027					1110457										919354	1182715			
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H0648: 1, L0747: 1, L0756: 1, L0779: 1, L0752: 1 and L0759: 1.					7, AR089:	H0039: 5, H0622: 5,	.0748: 4, H0667: 4,	126: 3,	278: 2,	618: 2,	H0318: 2, H0123: 2,	179: 2,	H0271: 2, S0036: 2,	634: 2,	100:2,	H0633: 2, S0210: 2,	144: 2,	L0438: 2, L0602: 2,	731: 2,	501: 2,	542: 2,	222: 1,	H0294: 1, H0583: 1,	657: 1,	H0484: 1, H0306: 1,	420: 1,	580: 1,
1, LO 1, LO 1 and): 5, H	4, H0	3, S0	2, S0	2, H0	2, H0	2, H0	2, S0	2, HC	2, HC	2, S0	2, H0	2, L0	2, L0′	2, L0	2, HC	1, HC	1, HC	1, HC	1, HC	1, S0	1, H0
H0648: 1, L0747: 1, L0756: 1, L0779: 1, L0752: 1 and L0759	т				AR061:	H0036	L0748:	H0255: 3, S0126: 3,	H0393:	H0599:	H0318:	H0050:	H0271:	H0135:	H0087:	H0633:	S0002:	L0438:	L0744:	L0595: 2, L0601: 2,	H0665: 2, H0542:	H0556:	H0294:	H0650: 1, H0657:	H0484:	S0418: 1, S0420: 1	S0354: 1, H0580:
	5,	φ,	9,	118.	3,	 	121,	59,	222,	285,	330,	364,	.07,	166,	187.												
	Gly-3	Pro-5	Met-9	Asp-	Ser-68	Gln-9	Asn-	Lys-1	Ala-	Asn-	Pro-	Ala-	Asp-4	. Val-4	Thr-4												
	Glu-29 to Gly-35,	Arg-53 to Pro-59,	Thr-88 to Met-99,	Pro-109 to Asp-118	Gly-59 to Ser-68,	Ala-87 to Glu-98,	Pro-106 to Asn-121,	Ser-148 to Lys-159,	Phe-207 to Ala-222,	Cys-279 to Asn-285,	Gly-322 to Pro-330,	Glu-357 to Ala-364,	Ile-402 to Asp-407,	Pro-456 to Val-466,	Ser-474 to Thr-487.												!
	Glu	Arg	Thr.	Pro-	Gly.	Ala-	Pro-	Ser-	Phe	Cys	<u>G</u>	Clin	IIe-7	Pro-	Ser-	<u>-</u>											
	1052				749																						
	473				745																_						
	7-06		- ,		3-1																						
	454			•	151																						
	921126				1219819																						
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					HAHGD33																						
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S0007: 1, S0046: 1, H0619: 1, H0550: 1,)2: 1, H0586: 1,	H0333: 1, H0486: 1,	22: 1, H0196: 1,	97: 1, H0544: 1,)9: 1, H0172: 1,	L0471: 1, H0023: 1,	H0071: 1, H0266: 1,		H0628: 1, H0551: 1,	H0056: 1, H0623: 1,		25: 1, H0561: 1,	H0386: 1, H0509: 1,	H0131: 1, H0130: 1,	H0646: 1, S0144: 1,	S0426: 1, H0529: 1,	L0565: 1, H0547: 1,	H0689: 1, H0435: 1,	H0670: 1, S0330: 1,	H0521: 1, S0027: 1,	S0028: 1, S0032: 1,	L0439: 1, L0747: 1,	L0759: 1, S0260: 1,	H0445: 1, L0597: 1,	,04: 1, L0593: 1,	L0366: 1, H0668: 1,	S0242: 1 and H0422: 1.	
S0007: H0619:	H03	H03	HOI	H0597:	H0009:	104	00H	H02	90H)OH	800)OH	H03	[0H]	90H	804	103)Н0	0H	HO	080	70T		HO	TO	ITO	08	3 Dhe_22 to Ala-37
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	H0039: 10664: 50779: 50779: 5	10667; 4H0618; 10438; 104485; 104485; 104485; 104485; 104485; 104485; 104485; 104485; 104485; 104485; 104485; 1044	_0602:	H0542: S0358: S0278:	H0333: H0318: H0123:	H0620: H0271: H0135:	H0087: H0633: S0002:	L0646: L0774: L0565:
	AKUSS: 5, AKUST: L0748: 8, H0039: 5, H0622: 5, L0664: 5, L0439: 5, L0779: 5, L0731: 5, L0758: 5,	L0665: 4, L0744: 4, L0601: 4, H0667: 4, H0255: 3, H0618: 3, L0666: 3, L0438: 3,	S0126: 3, L0602: 3, L0742: 3, L0604: 3,	L0595: 3, H0542: 3, H0265: 2, S0358: 2, H0393: 2, S0278: 2,	H0550: 2, H0333: 2 H0599: 2, H0318: 2 H0545: 2, H0123: 3	H0050: 2, H0620: 2, H0179: 2, H0271: 2, S0036: 2, H0135: 2,	H0634: 2, H0087: H0100: 2, H0633: S0210: 2, S0002:	L0769: 2, L0646: 2, L0768: 2, L0774: 2, H0144: 2, L0565: 2,
	<u>, </u>				HHH	N H H S	H H S	<u> </u>
Cys-94 to Asn-100, Gly-137 to Pro-145, Glu-172 to Ala-179, Ile-217 to Asp-222.	Gly-59 to Ser-68, Ala-87 to Glu-98, Pro-106 to Asn-121, Ser-148 to Lys-159, Phe-207 to Ala-222,	Ile-284 to Lys-289.						
Cys Gly Glu	Ala Pro Ser	Ile-				·		
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	3 - 908							
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H0689: 2, S0027: 2, L0747: 2, L0755: 2,	L0593: 2, H0665: 2,	56: 1, T0002: 1,	.22: 1, H0685: 1,	94: 1, S0430: 1,	H0583: 1, H0650: 1,	57: 1, S0212: 1,	82: 1, H0484: 1,	H0306: 1, S0418: 1,	80420: 1, 80354: 1,	S0360: 1, H0580: 1,	S0007: 1, S0046: 1,	519: 1, H0351: 1,	H0549: 1, H0392: 1,	H0586: 1, H0486: 1,	F0060: 1, L0022: 1,	H0122: 1, H0196: 1,	H0597: 1, H0544: 1,	H0009: 1, H0172: 1,	L0471: 1, H0023: 1,	H0071: 1, H0266: 1,	290: 1, S0022: 1,	H0030: 1, H0553: 1,	H0628: 1, H0182: 1,	517: 1, H0606: 1,	551: 1, H0413: 1,	H0056: 1, H0623: 1,	S0038: 1, H0494: 1,	H0625: 1, H0561: 1,	H0386: 1, H0509: 1,
H068	T059	H05	H02;	H02	H05	90H	8028	H03	S042	8036)00S	90H	H05	H05	T00	H01	H05	00H	L04	00H	H02	00H	90H	90H	HOS	00H	008	90H	H03
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H0131: 1, H0130: 1, H0646: 1, S0144: 1,	S0344: 1, S0426: 1,	10529: 1, L0763: 1,	L0770: 1, L0637: 1,	.0372: 1, L0662: 1,	L0775: 1, L0776: 1,	.0659: 1, L0383: 1,	.0790: 1, H0547: 1,	H0435: 1, H0658: 1,	H0670: 1, S0330: 1,	H0521: 1, H0436: 1,	30390: 1, S0028: 1,	30032: 1, L0750: 1,	L0753: 1, L0757: 1,	20759: 1, S0260: 1,	H0445: 1, H0595: 1,	20597: 1, L0366: 1,	H0668: 1, S0242: 1,	H0423: 1, H0422: 1 and	H0352: 1.	AR061: 9, AR089: 6	L0754: 6, H0318: 3,	H0486: 2, H0013: 2,	H0014: 2, L0439: 2,	L0777: 2, H0543: 2,	H0171: 1, H0556: 1,	S6024: 1, H0583: 1,	H0650: 1, H0638: 1,	S0354: 1, H0580: 1,
	<u> </u>			<u> </u>		. E-1 .					<u> </u>	<u> </u>								,	•		Arg-161 to Gly-168.					
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															-					1206665								
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H0619: 1, H0455: 1, H0009: 1, S0003: 1, L0483: 1, S0036: 1, H0591: 1, H0494: 1, S0014: 1, S0450: 1, L0520: 1, L0763: 1, L0769: 1, L0641: 1, L0769: 1, L0662: 1, L0776: 1, L0774: 1, L0776: 1, L0774: 1, H0520: 1, H0144: 1, H0520: 1, H0547: 1, H0519: 1, S0136: 1, H0519: 1, S0136: 1, H0519: 1, S0136: 1, H0521: 1, H0522: 1,		AR061: 2, AR089: 1 L0794: 7, L0743: 2, H0543: 2, S0040: 1, S0134: 1, S0356: 1, T0082: 1, H0251: 1, H0494: 1, H0625: 1, H0649: 1, L0806: 1,
S S C H H H C C C C S H C H H S S S S S	Glu-1 to Gly-7, Gln-43 to Arg-50, Asp-60 to Gly-67, Phe-150 to Glu-156, Arg-176 to Lys-181.	
	1 1054	361 752
	456 2 - 691	154 3 - 13
	921850 4	1219522 1
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L0657: 1, L0565: 1, L0758: 1, L0608: 1 and S0026: 1.		AR061: 3, AR089: 2	L0769: 5, L0774: 5,	S0358: 2, S0444: 2,	S0408: 2, H0587: 2,	L0764: 2, L0766: 2,	L0775: 2, L0601: 2,	H0170: 1, S0442: 1,	S0410: 1, H0497: 1,	H0333: 1, H0632: 1,	H0156: 1, L0022: 1,	L0738: 1, H0271: 1,	H0039: 1, S0344: 1,	L0637: 1, L0772: 1,	L0646: 1, L0773: 1,	L0662: 1, L0518: 1,	L0783: 1, L0791: 1,	L0663: 1, S0374: 1,	H0593: 1, H0660: 1,	H0648: 1, H0672: 1,	H0696: 1, L0749: 1,	L0750: 1, L0779: 1,	L0752: 1, L0755: 1,	L0599: 1 and H0667: 1.	
		Gly-1 to Arg-19,	Asp-27 to Glu-34,	Pro-63 to Arg-70.	Lys-97 to Lys-103,	Asp-113 to Gly-118,	Ala-148 to Tyr-158.																		Gly-25 to Arg-45, Asp-53 to Glu-60,
	1055	753																							1056
	196 - 1104	2 - 517				-	•	-		-															3 - 503
	457	155																							458
	922102	1127881																							922194
		HHGAE47																							
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			AR061: 8, AR089: 5	L0769: 5, L0774: 5,	.0756: 4, H0624: 2,	S0358: 2, S0444: 2,	S0408: 2, H0587: 2,)764: 2, L0766: 2,	.0775: 2, L0601: 2,	0170: 1, S0442: 1,	S0410: 1, H0497: 1,	H0333: 1, H0632: 1,	0156: 1, L0022: 1,	L0738: 1, H0271: 1,	0039: 1, S0344: 1,	L0637: 1, L0772: 1,	.0646: 1, L0773: 1,	L0662: 1, L0518: 1,	783: 1, L0791: 1,	.0663: 1, S0374: 1,	H0593: 1, H0660: 1,	H0648: 1, H0672: 1,	H0696: 1, L0749: 1,	20750: 1, L0779: 1,	20752: 1, L0755: 1,	
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Asp-66 to Lys-72,	Arg-89 to Trp-106, Asn-121 to Gly-147,	Val-152 to Gly-159,	Glu-8 to Pro-16,	Gln-21 to Glu-26,	Gly-105 to Arg-125	Asp-133 to Glu-140,	Asp-146 to Lys-152,	Pro-169 to Arg-176,	Lys-203 to Lys-209	Asp-219 to Gly-224,	Ala-254 to Tyr-264.															Gln-1 to Glu-10,
		•	754		-																					1057
			89 - 922		-																					442 - 885
			156																							459
			1165349														-									922195
			HMCGL45																							
			146																							

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	AR061: 1, AR089: 1 S0045: 1 and H0457: 1.		AR089: 4, AR061: 2	H0040: 1, H0052: 1,										AR061: 5, AR089: 2	L0747: 14, H0551: 9,	H0617: 7, S0022: 6,	H0135: 6, S3014: 6,	L0750: 6, L0757: 6,	L0759: 6, H0545: 5,	S0126: 5, H0124: 4,	H0529: 4, L0769: 4,	L0764: 4, L0665: 4,
Asp-16 to Lys-22, Pro-39 to Arg-46, Lys-73 to Lys-79, Asp-89 to Gly-94, Ala-124 to Tyr-134.	Ser-29 to Val-36, Leu-217 to Ser-222, Lys-255 to Ile-262.	Phe-21 to Lys-27.	Asp-11 to Val-21,	Tro-2/ to 1 nr-43,	Pro-136 to Gly-149,	Met-182 to Val-193,	Thr-197 to Asn-203.	Asp-11 to Val-21,	Pro-27 to Thr-43,	Trp-92 to Lys-97,	Pro-136 to Gly-149,	Met-182 to Val-193,	Thr-197 to Asn-203.	Asn-61 to Glu-70,	Ser-80 to Arg-85,		Gln-101 to Gly-109,					
	755	1058	756					1059						757								
	1310 - 501	53 - 625	3 - 704					3 - 704			• •			3 - 395								
	157	460	158					461						159								
	1153884	926930	1212235					927120						1165357				<u></u>				
	HELEF11		HETJX04											HSOBC04								
	147	-	148											149								

[2: 4,	51: 4,	94: 3,	51: 3,	50: 3,	75: 3,	58: 3,	40: 2,	50: 2,	41: 2,	20: 2,	53: 2,	30: 2,	L0662: 2,	83: 2,	54: 2,	, L0439: 2,	55: 2,	18: 1,	22: 1,	570: 1,	56: 1,	544: 1,	[23: 1,	03: 1,	10:1,	.12: 1,	H0048: 1,)59: 1,	50:1,
H0547: 4, S3012: 4,	L0740: 4, L07	H0624: 3, H0294:	L0717: 3, H0251: 3,	H0024: 3, S0250: 3,	H0100: 3, L0375: 3,	L0651: 3, L07	H0170: 2, S0040: 2,	H0583: 2, H0550: 2,	H0333: 2, H00	H0012: 2, H0620: 2,	H0284: 2, H0553: 2,	H0606: 2, H0130: 2,	L0641: 2, L06	L0650: 2, L07	L0666: 2, L06	L0744: 2, L04	L0751: 2, L0755: 2,	H0667: 2, S0418: 1,	80354: 1, 802	H0441: 1, H0370: 1	T0109: 1, H0156: 1,	H0318: 1, H0	H0546: 1, H0123:	L0471: 1, T00	H0014: 1, T0010: 1	H0266: 1, S0312:	H0428: 1, H0	H0413: 1, H0059:	H0560: 1, S0150:
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L0770: 1, L0639: 1, L0772: 1, L0773: 1, L0768: 1, L0649: 1, L0775: 1, L0653: 1, L0776: 1, L0657: 1, L0656: 1, L0659: 1, L0809: 1, T0068: 1, H0593: 1, H0689: 1, H0593: 1, H0539: 1, S0130: 1, H0539: 1, S0152: 1, L0743: 1, L0777: 1, H0595: 1, L0591: 1, L0601: 1, S0192: 1, S0242: 1, S0194: 1, S0196: 1 and H0352: 1.		AR089: 0, AR061: 0 L0748: 6, L0749: 6, L0803: 3, L0774: 3, L0775: 3, H0574: 1, H0632: 1, H0013: 1, L0789: 1, L0790: 1, H0144: 1 and L0581: 1.		AR089: 1, AR061: 0 S0354: 1 and L0596: 1.	AR051: 23, AR054: 11, AR050: 9, AR061:
	Asn-59 to Glu-67.	Glu-69 to Gln-76.	Glu-69 to Gln-76.	Pro-1 to Thr-8.	Ile-1 to Ser-16.
-	1060	758	1061	759	760
	2 - 388	1 - 546	1 - 546	100 - 408	143 - 514
	462	160	463	161	162
	927280	1069980	927532	927676	1129143
	1	HE8PW83 1	1	HWLEA48	HNHNP81
		150		151	152

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8, AR089: 5 S0216: 1		7, AR061:	2, AK054:	AR051: 1	S0192: 1			AR089: 8, AR061: 4	H0653: 2, H0650: 1,	H0050: 1, L0370: 1,	L0800: 1, L0662: 1,	L0653: 1, H0436: 1 and	L0749: 1.															
	Ile-1 to Ser-16.	Pro-18 to Pro-27,	Glu-6/ to Lys-/3,	Phe-147 to Tyr-165,	Thr-203 to Ser-209.	Glu-40 to Lys-46,	Phe-120 to Ser-132.	Gly-1 to Glu-7,	Lys-16 to Leu-21,	Ser-26 to Val-31,	Asp-64 to Thr-70,	Asp-131 to Asn-136,	Lys-191 to Asp-197,	Ala-259 to Glu-264,	Glu-273 to Gly-279,	Gln-296 to Ala-305,	Asn-317 to Ser-322,	Asn-345 to Ser-352,	Gln-384 to Asn-392,	Asn-407 to Gly-412,	Gly-434 to Pro-441,	Lys-476 to Asp-481,	Gln-497 to Asn-507,	His-523 to Asn-528.	Lys-10 to Leu-15,	Ser-20 to Val-25,	Asp-58 to Thr-64,	Asp-125 to Asn-130.
	1062	761				1063		762																	1064			
	143 - 514	1161 - 535				2 - 529		2 - 1618																	2 - 520			
	464	163				465	-	164																	466			
	928378	1123641				928475		1165261																	929264			
		HFIDL68						HUJCT05										•										
		153						154							_							<u> </u>						

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AR089: 1, AR061: 0	H0038: 2, L0745: 2	and H0616: 1.	AR089: 1, AR061: 0	H0620: 3, L0/94: 3,	S0212: 2, H0254: 2,	H0545: 2, H0266: 2,	.0639: 2, L0759: 2,	H0556: 1, H0657: 1,	S0418: 1, H0580: 1,	345: 1, H0619: 1,	H0550: 1, H0600: 1,	H0590: 1, H0253: 1,	H0581: 1, H0052: 1,	H0309: 1, H0085: 1,		H0617: 1, H0124: 1,	H0059: 1, H0494: 1,	S0144: 1, S0142: 1,	S0426: 1, H0529: 1,	796: 1, L0659: 1,	.0790: 1, H0519: 1,	H0711: 1, S0328: 1,	H0521: 1, H0522: 1,	S3014: 1, L0758: 1,	S0260: 1, H0343: 1,	S0434: 1, L0601: 1,	H0668: 1 and H0542: 1.	ı	AR061: 0, AR089: 0
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Pro-12 to Tyr-21.			Asp-35 to Leu-41,	Val-45 to Ser-57,	Glu-134 to Asp-139,	Pro-253 to Leu-259,	Ser-301 to Gly-306,	Leu-324 to Arg-330,	Val-374 to Tyr-381,	Gly-422 to Gly-427,	Gly-466 to Gly-481	Lys-500 to Asp-505,	Pro-540 to Asn-554,	Arg-610 to Ala-616,	Pro-773 to Ala-780.														Leu-49 to Tyr-54.
763			764								-																	1065	765
3 - 884			183 - 2591		•																							455 - 2239	124 - 324
165			166																									467	167
932583			1226719																									933364	934467
HTEG005 932583			HRDBH58 1																										HSDGW22
155			156																										157

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L0794: 4, L0438: 4, L0761: 3, L0766: 3, L0748: 3, L0439: 3, H0556: 2, L0602: 2, L0754: 2, L0779: 2, H0580: 1, H0208: 1, H0013: 1, T0082: 1, S0010: 1, H0428: 1, H0553: 1, H0038: 1, L0796: 1, L0800: 1, L0773: 1, L0533: 1, L0803: 1, L0776: 1, L0803: 1, L0776: 1, H0520: 1, H0519: 1, H0520: 1, H0187: 1, H0521: 1, S0031: 1 and L0731: 1, S0031: 1 and	AR089: 2, AR061: 2 H0519: 2, S0420: 1, T0114: 1, H0013: 1, S0346: 1, H0038: 1, S0142: 1, H0520: 1, H0521: 1 and H0136: 1.		AR061: 4, AR089: 2 H0052: 7, L0809: 4, H0663: 3, L0439: 3, L0752: 3, H0587: 2, L0565: 2, H0550: 1,
	Thr-1 to Gly-11, Thr-26 to Gly-34.		Arg-20 to Ala-25, Asp-56 to Val-62, Gln-88 to Ala-93, Thr-126 to Ala-132, Gln-142 to Asn-160,
	766	1066	767
	1 - 663	182 - 586	2 - 703
	168	468	169
	1126594	934522	1197900
	HNTMD79		HCESJS1
	158		159

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H0194: 1, H0562: 1, H0571: 1, L0435: 1, L0769: 1, L0787: 1 and L0755: 1.		AR089: 8, AR061: 3	L0803: 6, L0759: 6,	0740: 4, S0410: 3,	.0764: 3, L0766: 3,	304: 3, H0144: 3,)406: 3, L0731: 3,	362: 3, S0358: 2,)444: 2, H0596: 2,	H0644: 2, H0124: 2,	0770: 2, L0663: 2,	H0539: 2, L0747: 2,	0750: 2, L0779: 2,	0757: 2, L0758: 2,	0624: 1, H0171: 1,	0639: 1, L0717: 1,	H0411: 1, S0222: 1,	0441: 1, H0431: 1,	0574: 1, H0013: 1,	0156: 1, H0085: 1,	0471: 1, T0023: 1,	H0163: 1, H0130: 1,	20762: 1, L0763: 1,	.0662: 1, L0794: 1,	20775: 1, L0375: 1,	L0805: 1, L0659: 1,
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Ser-189 to Asn-196.	Pro-15 to Cys-22.	Val-57 to Tyr-65,	Asp-73 to Lys-81,	Arg-118 to Arg-12.	Asp-140 to Leu-147,	Pro-151 to Thr-156,	Ala-163 to Glu-168,	Pro-177 to Thr-187,	Asp-220 to Thr-229,	Thr-283 to Thr-289.			-													
	1067	89/																								
	227 - 781	3 - 947																								
	469	170																								
	934524	1151482								_										-						
		HHEFQ42	,																							
		160										_														

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L0783: 1, L0666: 1, S0374: 1, H0520: 1, H0658: 1, H0672: 1, S0330: 1, L0743: 1, L0751: 1, L0777: 1 and H0542: 1.		AR061: 9, AR089: 3	H0574: 1 and S0344: 1									AR061: 226, AR089:	79	L0439: 8, H0052: 7,	L0741: 7, L0756: 4,	S0010: 3, H0261: 2,	H0156: 2, S0049: 2,	L0770: 2, L0776: 2,	L0742: 2, L0745: 2,	L0366: 2, S0222: 1,	H0438: 1, H0390: 1,	S0346: 1, H0009: 1,	L0455: 1, S0038: 1,	L0789: 1 and L0758: 1.
		Gly-19 to Ile-27,	Thr-31 to Asp-41,	Asp-58 to Phe-67,	Ser-79 to Lys-85,	Leu-119 to Glu-127.	Gly-19 to Ile-27,	Thr-31 to Asp-41,	Asp-58 to Phe-67,	Ser-79 to Lys-85,	Leu-119 to Glu-127.	Ala-5 to Gly-13,	Pro-31 to Gln-37,	Ala-46 to Ala-69,	Tyr-81 to Ser-87,	Ser-120 to Ile-137,						Gln-365 to Ser-372.		
	1068	692					1069					770												
	29 - 1072	2 - 499					1 - 444					1 - 1119												
	470	171					471					172												
	934527	1082368					934528					1195825												
		HLQDC55										HFPHI62												
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		AR089: 3, AR061: 3	H0261: 1, H0013: 1,	H0052: 1, H0009: 1,	H0144: 1 and L0438: 1.			AR089: 12, AR061: 4	H0242: 2, S0040: 1,	S6024: 1, S6014: 1,	H0586: 1, H0013: 1,	10124: 1, L0756: 1,	L0592: 1, L0366: 1 and	H0542: 1.		AR051: 14, AR089: 6,	R061: 4, AR050: 2,	AR054: 2	L0744: 9, L0747: 8,	3014: 7, L0740: 7,	(0192: 6, S0027: 5,	S0212: 4, H0124: 4,	.0731: 4, L0662: 3,	,0743: 3, L0752: 3,	.0759: 3, H0662: 2,	0418: 2, S0046: 2,	H0575: 2, H0545: 2,	H0041: 2, H0413: 2,	L0775: 2, H0696: 2,
		V		,				V		S	正	正	ᆸ	<u> </u>		\ V	<u>∢</u>	<u>∢</u>		S						<u>\SS</u>	<u>;II;</u>	<u>11</u>	_
Met-1 to Gln-6,	Pro-38 to Asn-60.	Ala-46 to Ser-53,	Pro-63 to Leu-78,	Asp-106 to Asp-114,	Glu-129 to Leu-136,	Gly-144 to Asp-149.	Gly-4 to Thr-9.	Ala-108 to His-113,	Asp-149 to Asn-154,	Cys-179 to Val-186.					:	Ala-1 to Trp-9,	Pro-12 to Gln-17,	Arg-37 to Pro-42,	Thr-44 to Lys-51,	Pro-66 to Pro-80,	Thr-97 to Ala-106,	Pro-120 to Trp-128,	Leu-131 to Gly-137.						
1070		771					1071	772							1072	773													
3 - 410		1 - 597					2 - 625	1 - 585							2 - 565	157 - 681													
472		173		-			473	174							474	175													
934529		1152238					934532	1128791							934540	1182276													
		нЕ8ОН09						HFAAX29								HHFOC79													
		163						164								165													

48: 2, 54: 2, 58: 2, 76: 2, 78: 1,	91: 1, 40: 1, 27: 1, 42: 1, 05: 1, 544: 1,	200: 1, 112: 1, 41: 1, 533: 1, 552: 1, 59: 1, 83: 1,	44: 1, 26: 1, 135: 1, 572: 1, 55: 1, 77: 1, 34: 1,
37: 2, L07, 51: 2, L07, 49: 2, L07, 145: 2, S02, S24: 1, L07, L07, L07, L07, L07, L07, L07, L07	H0441: 1, H0391: 1, S0005: 1, T0040: 1, H0069: 1, H0427: 1, S0280: 1, H0042: 1, T0048: 1, H0505: 1, H0309: 1, H0544: 1,	H0009: 1, H0266: 1 H0617: 1, H0412: 1 H0623: 1, T0004: 1, L0564: 1, T0041: 1, H0494: 1, H0633: 1 H0646: 1, H0652: 1 L0769: 1, L0646: 1, L0655: 1, L0659: 1, L0546: 1, L0783: 1,	L0809: 1, H0144: 1 L0565: 1, S0126: 1, H0689: 1, H0435: 1 H0659: 1, H0672: 1 S0378: 1, H0555: 1 S0206: 1, L0777: 1, L0780: 1, S0434: 1, S0011: 1, S0194: 1 H0506: 1.
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		061: 0	7, 1,	7: 6,	9: 5,	9:3,	20: 2,	35: 2,	18: 2,	1:2,	4: 1,	87: 1,	81: 1,	77: 1,	41: 1,	29: 1,	52: 1,	74: 1,	6: 1,	17: 1,)1:1,	56: 1,	55: 1,	47: 1,	28: 1,	77: 1,	58: 1,	H0506: 1
		: 1, AR061	H0457: 8, L0766: 7,	.0599: 6, H0677: 6,	.0438: 5, L0779: 5,	H0012: 3, L0809: 3,	H0656: 2, H0620: 2,	.0771: 2, H0435: 2,	H0436: 2, L0748: 2,	.0439: 2, L0751: 2	.0749: 2, S0134:	H0645: 1, H0587:	H0635: 1, H0581:	: 1, H04	H0560: 1, H0641:	S0422: 1, H0529:	: 1, L0662:	: 1, L0774:	: 1, L0606:	: 1, L0647:	: 1, L0791:	: 1, L0666:	: 1, L0665:	:: 1, H0547:	H0576: 1, S0028: 1	.0756: 1, L0777: 1	.0755: 1, L0758: 1	H0543: 1 and H0506: 1.
		AR089:	H045	L0599:	L0438:	H0012	H0656	L0771:	H0436	L0439:	L0749:	H0645	H0635	H0546	H0560	S0422:	L0521: 1	L0794: 1,]	L0775: 1	L0659: 1,	L0789: 1	L0792: 1	L0663:	H0702:	H0576	L0756	L0755	H0543
15,	5-28, -47.	10,	-48,	,-66,	r-119,	la-147,	a-171,	p-227,	p-238,	lu-258,	er-270,	p-310,	he-335,	.u-349,	p-383,	ly-398,	rp-458,	rp-486,	ly-505,	lu-573,	ne-618,	rg-697,	lu-742,	sp-802,	hr-827,	s-849,	ly-860,	yr-886,
Glu-6 to Glu-15,	Thr-21 to Asp-28, Ser-42 to Lys-47.	Gly-1 to Trp-10,	Glu-12 to Thr-48,	Phe-94 to Gly-99	Tyr-105 to Ser-119	Thr-136 to Ala-147,	Ser-165 to Ala-171,	Glu-222 to Trp-227,	His-233 to Trp-238,	Glu-251 to Glu-258,	Asn-265 to Ser-270,	Gln-305 to Trp-310,	Asn-325 to Phe-335,	Ser-341 to Glu-349,	Lys-378 to Trp-383,	Ala-390 to Gly-398,	Asn-451 to Trp-458,	Met-476 to Trp-486,	Gln-497 to Gly-505,	Arg-567 to Glu-573,	Gln-610 to Phe-618,	Glu-687 to Arg-697,	Gly-732 to Glu-742,	Thr-797 to Asp-802,	Arg-818 to Thr-827,	Ile-840 to Lys-849,	Ala-853 to Gly-860,	Pro-879 to Tyr-886,
Glu-6	Thr-2 Ser-4	Gly-1	Glu-1	Phe-9	Tyr-1	Thr-1	Ser-1	Glu-7	His-2	Glu-7	Asn-	Gln-	Asn-	Ser-3	Lys-3	Ala-	Asn-	Met-	Glu-	Arg-	Gln-(Gln-	<u>Gly-,</u>	Thr.	Arg-	Ile-8	Ala-8	Pro-{
1073		774																										
- 443		2970																										
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475		176																										
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					AR089: 1, AR061: 0	L0769: 3, H0052: 2,	L0439: 2, H0572: 1,	H0015: 1, L0438: 1 and	L0741: 1.	AR061: 7, AR089: 4	H0551: 3, H0529: 3,	L0769: 3, L0758: 3,	S0418: 2, L0770: 2,	L0773: 2, L0521: 2,	H0701: 2, S0126: 2,	L0747: 2, L0731: 2,	L0759: 2, L0589: 2,	L0601: 2, H0624: 1,	H0149: 1, H0556: 1,	H0295: 1, S0134: 1,	H0583: 1, H0661: 1,	H0592: 1, H0013: 1,	H0635: 1, H0581: 1,	S0250: 1, H0212: 1,	H0412: 1, S0144: 1	L0763: 1, L0645: 1,	L0764: 1, L0794: 1,	L0766: 1, L0775: 1,	L0783: 1, L0665: 1,
Ser-893 to Ile-901,	Thr-904 to Phe-911,	Asp-931 to Pro-93/,	Arg-952 to Thr-962.	Glu-1 to Thr-13.	Pro-26 to Tyr-31.					His-12 to Arg-20,	Pro-26 to Asp-43,	Ala-62 to Glu-70,	Arg-78 to Arg-83,	Phe-100 to Gln-105,	Gly-129 to Glu-136,	Met-182 to Ile-187,	Tyr-277 to Ala-284.	•											
	-			1074	775					2776																			
				1 - 150	810 - 289					52 - 966		-																	
				476	177					178																			
				935465	938398					1178621																			
					HCECQ23					HTGAU79																			
					167					168																			

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H0519: 1, H0435: 1, H0672: 1, H0436: 1, S3014: 1, S0028: 1, L0750: 1, L0777: 1, L0366: 1, H0667: 1 and H0423: 1.			AR061: 6, AR089: 2	L0749: 2, H0144: 1		AR051: 9, AR054: 9,	AR050: 7, AR061: 3,	AR089: 2	H0271: 26, H0521: 26,	H0046: 20, L0747: 20,	S0278: 14, S0052: 14,	L0754: 12, L0599: 12,	S0142: 11, S0428: 11,	H0179: 10, S0344: 10,	L0776: 9, H0638: 8,	L0771: 8, L0666: 8,	S0360: 7, S0144: 7,	L0775: 7, L0659: 7,	H0422: 7, S0354: 6,
	His-12 to Arg-20, Pro-26 to Asp-43, Ala-62 to Glu-70,	Arg-78 to Arg-83, Phe-100 to Gln-105, Gly-129 to Glu-136.	Glu-65 to Pro-70.			Gly-16 to Asn-21.													
	1075		777		1076	778													
	63 - 977		2 - 286		3 - 434														
	477		179		478	180													
	940369	:	1156432		941348	565781													
			HE9FI33			HNHCP79													
			169			170													

H0580: 6, H0622: 6, H0641: 6, H0522: 6	T 0740: 6, T 0505: 6	HOS81: 5 HO416: 5	H0673: 5, L0598: 5,	L0774: 5, S3014: 5,	L0777: 5, L0759: 5,	L0362: 5, H0423: 5,	H0069: 4, H0674: 4,	L0770: 4, L0769: 4,	L0750: 4, L0752: 4,	L0731: 4, L0757: 4,	L0603: 4, S0114: 3,	S0134: 3, S0116: 3,	H0341: 3, S0418: 3,	S0358: 3, H0545: 3,	H0050: 3, H0646: 3,	L0768: 3, L0664: 3,	S0053: 3, S0216: 3,	S0374: 3, S0404: 3,	S0206: 3, L0745: 3,	L0756: 3, L0581: 3,	H0170: 2, H0222: 2,	L0785: 2, H0663: 2,	S0376: 2, S0132: 2,	S0222: 2, H0370: 2,	H0486: 2, H0013: 2,	H0635: 2, S0280: 2,	H0575: 2, H0036: 2,	H0618: 2, H0597: 2,	H0014-2 H0039-2
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L0142: 2, H0551: 2,	H0056: 2, H0561: 2,	S0426: 2, L0763: 2,	L0761: 2, L0648: 2,	L0662: 2, L0767: 2,	L0655: 2, L0519: 2,	L0665: 2, H0519: 2,	H0435: 2, H0696: 2,	S0027: 2, L0743: 2,	L0751: 2, S0031: 2,	S0260: 2, H0445: 2,	S0434: 2, L0590: 2,	S0276: 2, H0395: 1,	H0556: 1, T0002: 1,	H0685: 1, S0040: 1,	H0294: 1, S0218: 1,	S0001: 1, H0484: 1,	H0483: 1, H0662: 1,	H0176: 1, H0589: 1,	H0459: 1, S0356: 1,	S0408: 1, S0410: 1,	L0717: 1, H0411: 1,	H0549: 1, H0550: 1,	H0431: 1, H0608: 1,	H0409: 1, H0404: 1,	H0587: 1, H0485: 1,	H0250: 1, L0021: 1,	H0590: 1, H0318: 1,	T0071: 1, H0421: 1,	H0263: 1, H0596: 1,	H0150: 1, H0009: 1,
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L0471: 1, H0011: 1, S0051: 1, H0083: 1, H0510: 1, H0594: 1,	H0286: 1, S0250: 1,	H0328: 1, H0553: 1, L0055: 1, H0032: 1,	H0169: 1, H0316: 1,	H0135: 1, H0090: 1,	H0591: 1, H0634: 1,	H0413: 1, H0623: 1,	H0059: 1, T0069: 1,	S0038: 1, H0100: 1,	T0041: 1, H0509: 1,	S0150: 1, H0633: 1,	S0002: 1, H0529: 1,	L0762: 1, L0667: 1,	L0772: 1, L0646: 1,	L0643: 1, L0521: 1,	L0766: 1, L0389: 1,	L0653: 1, L0629: 1,	L0527: 1, L0657: 1,	L0517: 1, L0384: 1,	L0809: 1, L0663: 1,	H0144: 1, H0697: 1,	S0126: 1, H0690: 1,	H0670: 1, H0648: 1,	S0378: 1, S0380: 1,	H0518: 1, S0152: 1,	S0013: 1, S0044: 1,	H0214: 1, H0555: 1,
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H0436: 1, H0478: 1, S0432: 1, S3012: 1, S0032: 1, L0744: 1, L0439: 1, L0779: 1, L0758: 1, S0308: 1, S0436: 1, L0593: 1, S0011: 1, H0543: 1 and S0458: 1.	T		AR061: 0, AR089: 0	H0618: 64, H0253: 52,	L0758: 6, L0779: 2,	H0392: 1, H0038: 1,	L0761: 1, L0803: 1,	L0806: 1 and L0697: 1.								AR061: 1, AR089: 1	S0222: 3, H0052: 3,	L0361: 3, H0179: 2,	L0769: 2, H0521: 2,	H0555: 2, L0779: 2,	L0758: 2, H0663: 1,	H0549: 1, S0220: 1,
			Pro-3 to Gly-8,	Val-21 to Gly-30,	Gly-68 to Ala-85,	His-94 to Gly-99,	Ala-105 to Arg-110,	Ala-114 to Gln-138,	Arg-143 to Glu-155,	Leu-202 to Arg-222,	Arg-287 to Ser-292,	Pro-325 to Arg-332,	Arg-337 to Gly-351,	Val-388 to Lys-396.		His-9 to Ile-15.						
	1077	1078	622												1079	780						
	138 - 275	2 - 748	164 - 1351												1 - 1368	289 - 651						
	479	480	181												481	182						
	775293	941862	1194806												942161	942527						
			HTLIY52													HRAED74						
			171													172						

, H0156: 1, , H0596: 1, , T0010: 1, , L0143: 1, , L0794: 1, , L0809: 1, , L0747: 1, , L0780: 1,	AR089: 2 H0024: 2, 0222: 1, I0123: 1,	and S0052: 1.				AR089: 5 20803: 3, 0743: 2,	0785: 1,
H0586: 1, H0156: 1, S0010: 1, H0596: 1, S0051: 1, T0010: 1, H0271: 1, L0143: 1, L0764: 1, L0794: 1, L0806: 1, L0809: 1, H0518: 1, H0478: 1, L0750: 1, L0747: 1, L0750: 1, L0780: 1,	AR061: 6, AR089: H0620: 2, H0024: 2, H0208: 1, S0222: 1, H0194: 1, H0123: 1,	AR061: 7, AR089:	H0616: 1			AR061: 5, AR089: S0356: 9, L0803: 3, L0766: 2, L0743: 2,	L0731: 2, L0785: 1,
	Thr-9 to Val-16.	His-3 to Ser-14,	Thr-20 to Ser-27, Pro-41 to Asn-50, Glu-101 to Asp-109,	Ala-1 to Gln-7,	Cys-2+ to Sct-59, Pro-44 to Asn-53, Glu-104 to Asp-112, Leu-152 to Ser-157	Thr-1 to Leu-9, Pro-34 to Lys-40, Glu-82 to Gln-87,	Ala-216 to His-233,
	781	782		1080		783	
	145 - 684	462 - 962		454 - 963		210 - 1511	
	183	184		482		185	
	943757	1205381		944419		1206797	
	HFKKN77	HTEMU66				HWAGU62	
	173	174				175	

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S0116: 1, S0354: 1, S0358: 1, S0278: 1, H0642: 1, H0486: 1, H0581: 1, H0596: 1, H0355: 1, S0003: 1, L0455: 1, R0409: 1, H0591: 1, S0142: 1, S0344: 1, S0422: 1, S0346: 1, L0598: 1, L0794: 1, L0804: 1, L0659: 1, L0789: 1, L0664: 1, H0547: 1, H0660: 1, S0330: 1, L0758: 1, L0779: 1, L0758: 1, L0608: 1,		AR061: 6, AR089: 3	H0455: 2, L0803: 2,	L0439: 2, L0745: 2,	S0282: 1, S0400: 1,	50346: 1, H0509: 1,	L0769: 1, L0438: 1,	L0756: 1 and S0106: 1.			
Met-235 to His-243, Pro-322 to Lys-327, Arg-346 to Trp-351.	Pro-100 to Lys-106, Glu-148 to Gln-153.	Glu-62 to Tyr-67, Pro-169 to 1 yrs-179		•	Tyr-324 to Asn-331,		His-393 to Ala-399,	Asp-420 to Asn-425,	Thr-460 to Lys-473,	Ser-488 to Gly-502.	Pro-36 to Lys-46,
	1081	784									1082
	1 - 1500	93 - 1643									1613 - 462
	483	186									484
	945368	1198036									946170
·		HFPFB39									
		176									

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	AR061: 3, AR089: L0754: 3, H0644: 2, L0803: 2, L0748: 2, H0620: 1, H0031: 1, L0774: 1 and L0789:		AR061: 2, AR089: 2 L0439: 11, L0794: 5, L0666: 5, S0222: 4, H0052: 3, L0756: 3, H0624: 2, S6028: 2, S0038: 2, L0638: 2, L0805: 2, L0664: 2, L0438: 2, L0740: 2, H0171: 1, S6024: 1, H0013: 1, H0374: 1, H0050: 1, S0386: 1, L0769: 1, L0768: 1, L0776: 1, L0659: 1, L0776: 1, L0659: 1, L0776: 1, and L0746: 1	JAR051: 15, AR050:
Pro-56 to Ala-68, Ala-85 to Arg-90, Tyr-191 to Asn-198, Gly-219 to Val-224, Leu-232 to Lys-238, His-260 to Ala-266.	Pro-128 to Ser-134.	Leu-143 to Thr-149, Gln-152 to Glu-157.	i .	Pro-1 to Asp-16,
	785	1083	786	787
	3 - 410	992 - 495	125 - 652	1 - 1029
	187	485	188	189
	1165993	946252	946830	1152417
	HPMFI38			HOFMS43
	177		178	179

AR089: 7, AR061: 5, AR054: 1 H0415: 1					AR089: 3, AR061: 2	S6016: 1 and H0428: 1.							AR061: 4, AR089: 1	L0758: 7, L0768: 2,	H0616: 1 and L0151: 1.			
Pro-60 to Asn-65, Tyr-83 to Tyr-89, Ser-102 to Pro-115, Pro-130 to Glu-141, Ser-151 to Glu-160, Trp-177 to Glu-183, Phe-191 to Arg-198, Phe-203 to Tyr-209, Asn-234 to Ala-240, Pro-266 to Pro-271, Ser-276 to Thr-311,	Asp-1 to Asp-17,	Pro-61 to Asn-66,	Tyr-84 to Tyr-90,	Ser-103 to Trp-110.	Arg-78 to His-85,	Leu-99 to Lys-104,	Lys-123 to His-132,	Thr-164 to Pro-171.	Arg-78 to His-85,	Leu-99 to Lys-104,	Lys-123 to His-132,	Ser-157 to Pro-174.	Tyr-1 to Lys-8,	Phe-19 to Ser-24,	Thr-28 to Ser-34,	Pro-54 to Trp-70,	Leu-110 to Asn-118,	Ser-145 to Asp-151,
	1084				788				1085				789					
	3 - 359				3 - 563				3 - 539				1 - 762					
·	486				190				487				191					
	947973				1091087			-	666246				1105272					
					HOVC014				,				HTEPE35					
					180								181					

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						AR061: 6, AR089: 1	L0752: 5, H0013: 2,	L0780: 2, H0624: 1,	H0170: 1, H0645: 1,	H0318: 1, L0750: 1,	L0779: 1 and L0777: 1.							AR061: 1, AR089: 0	S0040: 1, S0222: 1,	L0471: 1 and L0517: 1.		AR089: 3, AR061: 1	L0747: 12, L0755: 12,	L0766: 9, L0438: 9,	L0754: 7, H0046: 6,	L0751: 6, L0752: 6,	H0068: 5, L0775: 5,	L0439: 5, S0010: 4,	JH0547: 4, S0152: 4,
Pro-162 to Val-172,	Pro-180 to Thr-185.	Tyr-1 to Lys-8,	Phe-19 to Ser-24,	Thr-28 to Ser-34,	Pro-54 to Trp-70.	Pro-22 to Gly-32,	Arg-52 to Gly-60,	Ser-78 to Met-89,	Ile-100 to Ser-106,	Asp-130 to Leu-137,	Tyr-146 to Ala-151.	Pro-22 to Gly-32,	Arg-52 to Gly-60,	Ser-78 to Met-89,	lle-100 to Ser-106,	Asp-130 to Leu-137,	Tyr-146 to Ser-152.	Ser-50 to Glu-62.			Ser-50 to Ser-66.	Pro-1 to Ala-12,	lle-264 to Val-277,	Gln-304 to Gln-309,	Ile-324 to Leu-330.				
		1086				790						1087						791			1088	792							
		839 - 78				1 - 1728						1 - 615						1-1188			1 - 243	3 - 1073							
		488	·			192						489						193			490	194							
		948475		_		1229490						948509						1090776			948519	1165229							
						HE8UA52												HOUBE50 1090776	_			HAJAV28							
						182												183				184							

L0740: 4, L0779: 4, L0779: 4, L0779: 4, L0759: 4, H0591: 3, L0771: 3, L0660: 3, S0028: 3, L0774: 3, L0660: 3, S0028: 3, L0748: 3, L0756: 3, L0756: 3, L0756: 3, L0756: 3, L0756: 3, L0757: 3, H0624: 2, S0045: 2, H0619: 2, S0045: 2, H0619: 2, S0036: 2, L0769: 2, L0776: 2, L0776: 2, L0659: 2, L0776: 2, L0659: 2, L0776: 2, L0659: 2, L0594: 2, L0594: 2, L0360: 1, H06171: 1, H0688: 1, S0040: 1, H0648: 1, H0648: 1, S0360: 1, S0408: 1, H0645: 1, H0645: 1, H0645: 1, H0650: 1, H0645: 1, H0650: 1, H0648: 1, L0106: 1, H0650: 1, H0648: 1, L0106: 1, H0659: 1, H0648: 1, L0106: 1, H0659: 1, H0648: 1, L0106: 1, H0659: 1, H0648: 1, H0648

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L0163: 1, H0594: 1, H0266: 1, H0290: 1, S0214: 1, H0328: 1, H0688: 1, H0622: 1, H0674: 1, S0364: 1, H0674: 1, S0364: 1, H0551: 1, T0067: 1, H0268: 1, H0100: 1, H0268: 1, L0763: 1, L0762: 1, L0763: 1, L0773: 1, L0521: 1, L0568: 1, H0144: 1, S0126: 1, H0144: 1, S0126: 1, H044: 1, S0126: 1, H0436: 1, H0555: 1, H0436: 1, H0555: 1, L0779: 1, H0550: 1, S0330: 1, L0741: 1, L0749: 1,	L0758: 1, 2077: 1, L0758: 1, S0026: 1 and H0506: 1.		AR061: 9, AR089: 6
100円 100円	0H	Pro-1 to Ala-12.	Pro-43 to Asn-61, AR
		1089 F	793 F
		3 - 464	54 - 1034
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L0659: 4, L0758: 4, L0777: 3, S0360: 2, L0775: 2, L0750: 2, L0731: 2, H0295: 1, S0218: 1, H0255: 1, H0402: 1, L0717: 1, H0641: 1, H0015: 1, H0673: 1, H0087: 1, L0770: 1, L0769: 1, L0646: 1, L0769: 1, L0655: 1, L0776: 1, L0655: 1, L0776: 1, H0683: 1, S0027: 1, H0683: 1, S0027: 1, L0748: 1, L0779: 1 and L0757: 1.		AR061: 5, AR089: 4 S0045: 2	AR061: 11, AR089: 3 L0748: 3, H0144: 2, H0632: 1 and L0581: 1.		AR061: 4, AR089: 3 H0590: 7, L0754: 5, H0156: 3, L0731: 3, L0600: 3, S0360: 2, H0339: 2, S0472: 2, L0803: 2, L0751: 2,
Ala-77 to Arg-82, Glu-207 to His-212, Glu-252 to Glu-261, Asp-279 to Asn-284.	Ala-20 to Arg-25.	Thr-16 to Pro-21.			Ile-25 to Asn-36, Glu-54 to Val-63, Gly-81 to Glu-86, Gly-108 to Thr-114, Val-125 to Ser-131.
	1090	794	795	1001	796
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	492	196	197	493	198
	949061	949067	1127726	949080	1128280
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T S S S H H T H H H H H H H H H H H H H	Ile-25 to Asn-36, Glu-54 to Val-63,
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		AR061: 2, AR089: L0637: 2, L0783: 2,	L0777: 2, S6022: 1,	H0392: 1, H058	H0050: 1, L0809: 1, L0759: 1 and S0192: 1	AR051: 744, AR054	681, ARUSU: 564, AR061: 2, AR089:	S0192: 3, H05	L0766: 1, L0804: 1,	H0521: 1 and L	AR089: 3, AR061: 3	L0438: 3, L0439: 3,	L0749: 3, L075	L0/66: 2, L03/5: 2, 1 0731-2 1.0759: 2.	L0803: 1, L065	L0517: 1, L066	L0664: 1, H0518: 1,	L0/48: 1, L0/79: 1, T 0509: 1 and H0008:					
Gly-81 to Glu-86,	Gly-108 to 110^{-114} , Val-125 to Ser-131.	Leu-9 to Leu-18, Ala-49 to Gly-55,	Gly-66 to Glu-74,	Ala-95 to Gln-100.							Arg-18 to Pro-23,	Pro-25 to Gly-37,	Ile-48 to Ile-61,	Asp-69 to Gly-74, $\frac{1}{100}$	Ser-105 to Asir-112:				Aro-34 to Pro-39.	Pro-41 to Gly-53,	Ile-64 to Ile-77,	Asp-85 to Gly-90,	Ser-121 to Asn-128.
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		1473 - 916				819 - 295					1 - 366								212 100	001 - 616			
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Asp-1 to Cys-10, Glu-31 to Pro-38, Met-43 to Val-48, Asp-97 to Phe-110, Asp-119 to Gly-137.	Asp-17 to Cys-26, Glu-47 to Pro-54, Met-59 to Val-64, Asp-113 to Phe-126, Asp-135 to Gly-153.	Ser-20 to Gly-32, Ile-43 to Ile-56, Asp-64 to Gly-69, Ser-100 to Asn-107.	Phe-1 to Trp-6, Ser-41 to Arg-56, Pro-162 to Leu-174.	Ser-7 to Gly-14, Leu-22 to Ala-28, Thr-57 to Ser-62.	Ser-85 to Arg-90, His-99 to Met-105, Met-119 to Val-125, Lys-127 to Ile-133,
800	1094	1095	801	1096	802
2 - 541	11 - 937	469 - 119	539 - 3	84 - 572	2 - 1306
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1129137	945039	950885	1144323	951518	1143411
HKGDE58 1129137			HCHMW40 1144323		HE8QZ34
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L0744: 2, L0439: 2, H0170: 1, H0013: 1, H0599: 1, S0182: 1, H0051: 1, H0510: 1, S6028: 1, L0455: 1, H0616: 1, S0422: 1, S0374: 1, L0438: 1, S0390: 1, L0748: 1 and L0604: 1.	1					AR089: 17, AR061: 8	L0789: 4, L0758: 4,	H0657: 3, H0052: 3,	L0438: 3, L0744: 3,	L0779: 3, L0005: 2,	H0581: 2, H0194: 2,	H0046: 2, H0038: 2,	L0800: 2, L0659: 2,	H0521: 2, L0743: 2,	L0439: 2, H0556: 1,	S0282: 1, S0358: 1,	H0619: 1, H0586: 1,	H0618: 1, H0231: 1, S0362: 1, H0622: 1.
Lys-215 to Tyr-221, Phe-239 to Lys-247, Asn-293 to Asp-298, Gln-404 to Tyr-411.	Ser-85 to Arg-90, His-99 to Met-105,	Met-119 to Val-125,	Lys-12/ to 11e-133,	Phe-239 to Lys-247,	Asn-293 to Gly-298.	Gln-103 to Asp-113,	Ser-182 to Phe-200,	Cys-211 to Ser-221,	Gln-233 to Ala-238,	Glu-256 to Ser-264.								
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T0006: 1, H0616: 1, H0413: 1, H0623: 1, L0351: 1, S0150: 1, L0769: 1, L0372: 1, L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0547: 1, H0672: 1, H0539: 1, S0378: 1, H0559: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1.						AR089: 15, AR061: 9	L0766: 4, L0745: 3,	L0752: 3, S0360: 2,	L0748: 2, L0746: 2,	L0755: 2, H0624: 1,	S0114: 1, H0098: 1,	L0471: 1, H0083: 1,	H0428: 1, L0483: 1,	H0090: 1, H0616: 1, H0494: 1, H0560: 1,
	Gln-110 to Asp-120,	Ser-189 to Phe-207,	Cys-218 to Ser-228,	Gin-240 to Ala-245,	Glu-263 to Ser-2/1.	Pro-19 to Gly-24,	Val-41 to Phe-47,	Lys-75 to Asp-83,	Ser-138 to Gln-154,	Asp-230 to Ser-235,	Asp-278 to Thr-283,	Pro-315 to Ser-324,	Trp-338 to Thr-344.	
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H0509: 1, L0761: L0772: 1, L0803: 1 L0776: 1, L0655: 1 L0792: 1, L0438: 1 H0520: 1, H0648: S0152: 1, H0648: S0152: 1, H0648: L0756: 1, L0779: L0758: 1, L0759: H0667: 1, H0543: L0465: 1.		9, AI	7, LO	, L07	H04	, L08	, L04	L05	, S00	H05	H03	, H00	H0375: 1, L0055:	S0036: 1, H0059:	S0038: 1, H0494: 1	S0002: 1, L0809: 1 0789: 1 - 1 0663:
10509: 1, 10772: 1, 10772: 1, 10772: 1, 10792: 1, 10520: 1, 10435: 1, 10478: 1, 10478: 1, 10558: 1, 10667: 1, 10667: 1, 10665:		:68	777:7	56: 4	<i>3</i> 2: 4,	52:3	87:2	49: 2,	59: 1	17: 1,	10: 1,	94: 1	75: 1	36: 1,	38: 1,)2: 1, %: 1,
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		Leu-89 to Tyr-96,	Leu-195 to Glu-209,	Val-253 to Ser-259,	Ile-274 to Phe-279	Lys-317 to His-323	ys-33	Ile-361 to Ser-366,	Glu-370 to Gln-375,	Lys-398 to Lys-404,	al-48	Met-539 to Glu-548,	Gly-573 to Tyr-578.			
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		Thr-9 to Val-16.					!	Ala-6 to Pro-12,	Glu-22 to Ala-41,	Ser-230 to Ala-238,	Asp-257 to Ser-268.		His-13 to Asn-24,	Pro-147 to Asn-157,	Gln-164 to Glu-169.	Ile-258 to Val-271,	Gln-298 to Gln-303,	Ile-318 to Leu-324,	Glu-353 to Leu-361,	Ser-397 to Arg-408,	Gly-427 to Leu-433.	
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	953622	955614						1189002				956115	965956			1187749						
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L0740: 4, L07/9: 4, L0759: 4, H0591: 3,	L0771: 3, L0662: 3,	L0774: 3, L0666: 3,	S0028: 3, L0/46: 3,	L0/56: 3, L0/31: 3, 1 0757: 3 H0624: 2	S0045: 2, H0619: 2,	S0222: 2, S0049: 2,	H0052: 2, H0615: 2,	S0036: 2, T0041: 2,	H0509: 2, S0002: 2,	S0426: 2, L0769: 2,	L0776: 2, L0659: 2,	H0521: 2, H0707: 2,	L0594: 2, L0362: 2,	S0011: 2, H0170: 1,	H0171: 1, H0685: 1,	S0040: 1, T0049: 1,	H0657: 1, S0001: 1,	H0638: 1, S0358: 1,	S0360: 1, S0408: 1,	H0637: 1, S0007: 1,	S0132: 1, S6022: 1,	H0550: 1, H0431: 1,	H0455: 1, H0574: 1,	H0486: 1, T0114: 1,	H0250: 1, H0069: 1,	H0156: 1, L0105: 1,	H0597: 1, H0546: 1,	H0545: 1, H0050: 1,
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Ile-316 to Leu-322, Glu-351 to Leu-359, Ser-395 to Arg-406, Gly-425 to Leu-431.	
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H0555: 1, L0754: 1	: 1, L078	L0596: 1, S0192: 1	H0542: 1 and H0423:	AR061: 7, AR089	L0769: 9, S0051: 4,	H0441: 3, S0036: 3,	L0809: 3, L0789: 3,	: 3, L04	: 3, H00	7: 2, H01	: 2, L07	: 2, L07	L0742: 2, L0756: 2,	: 2, H01	5: 1, S60	S0029: 1, H0411: 1	: 1, H04	H0486: 1, L0109: 1	H0251: 1, L0163:	H0617: 1, H0413:	:: 1, L0638:): 1, L0761:	i: 1, L06	1; 1, L0807:	L0657: 1, S0053: 1,	5: 1, H06	.0747: 1, L0757: 1,): 1, LO5	3: 1.
H0555	L0747	T0596	H0542	AR061	L076	H0441	L0809	L0438	L0731	H0687	T0800	T0665	L0742	S0031	H0556	S0029	S0278	H0486	H0251	H0617	L0762:	L0639: 1	L0764: 1	L0774:	L0657	S0126	L0747	L0759	L0608:
				6,	n-25,	y-75,	s-97,	yr-112,	'al-146,	sp-173.	ı																		
				Ala-1 to Lys-6,	Leu-13 to Gln-25,	Asp-70 to Gly-75,	92 to Ly	Asp-106 to Tyr-112,	Leu-135 to Val-146,	Glu-165 to Asp-173.																			
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1103 Arg-1 to Lys-13, Leu-20 to Gln-32, Asp-77 to Gly-82, Gly-99 to Lys-104, Asp-113 to Tyr-119, Leu-142 to Val-153, Glu-172 to Asp-180. H0013: 1 and S0027 1163590 214 1 - 492 812 Glu-172 to Asp-180. H0013: 1 and S0027 960914 506 111 - 455 1104 AR061: 1, AR069: 1128919 216 2 - 841 814 Leu-2 to Lys-10, AR061: 10, AR089: 1128919 216 2 - 841 814 Leu-2 to Lys-10, AR061: 10, AR089: 1128919 216 2 - 841 814 Leu-2 to Lys-10, AR061: 3, AR089: 1128919 216 2 - 841 814 Leu-2 to Lys-10, AR061: 1, AR089: 1198811 507 2 - 421 1105 Ala-1 to Met-18, L0731: 1 and L0596: 1194828 217 3 - 659 815 Asp-1 to Thr-7, AR089: 4, AR061: 3, Los-61, and Cofy-10. 1194828 217 3 - 659 815 Asp-1 to Thr-7, AR089: 4, AR061: 3, Lys-61 to Gly-66, S0212: 3, L0775: 3, Gly-112 to Leu-120, L0740: 3, H0566: 2, Glu-134 to Tyr-150, L0809: 2, H0696:																										
959160 505 2 - 583 1103 Arg-1 to Lys-13, Leu-20 to Gln-32, Asp-77 to Gly-82, Gly-99 to Lys-104, Asp-113 to Tyr-119, Leu-142 812 Glu-172 to Asp-180. 1163590 214 1 - 492 812 Glu-172 to Asp-180. 1128919 216 2 - 841 814 Leu-2 to Lys-10, Pro-87 to Pro-43, Ser-63 to Thr-79, T					·	1:1:		9	3							· <u>-</u>					1					
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959160 505 2 - 583 1163590 214 1 - 492 960914 506 111 - 455 962113 215 3 - 278 1128919 216 2 - 841 963811 507 2 - 421	Arg-1 to Lys-13, Leu-20 to Gln-32,	Asp-77 to Gly-82,	Gly-99 to Lys-104,	Asp-113 to Tyr-119,	Leu-142 to Val-133, Glu-172 to Asp-180.				Leu-2 to Lys-10,	Ala-29 to Pro-43,	Ser-63 to Thr-79,	Pro-87 to Pro-104.		Ala-1 to Met-18,	Leu-20 to Asn-26,	Val-38 to Leu-46,	Pro-48 to Gly-53,	Leu-81 to Gly-86,	Gln-94 to Tyr-99,	Glu-101 to Gly-109.	Asp-1 to Thr-7,	Asp-36 to Phe-51,	Lys-61 to Gly-66,	Gly-112 to Leu-120,	Glu-134 to Tyr-150,	Arg-193 to Lys-205.
959160 505 2- 1163590 214 1- 960914 506 111 962113 215 3- 1128919 216 2- 1128919 216 2- 1194828 217 3- 1194828 217 3-	1103					812	1104	813	814					1105							815					
959160 1163590 960914 962113 1128919 1194828						1 - 492	111 - 455		2 - 841																	
<u></u>	505					214	506	215	216					507							217					
	959160					1163590	960914	962113	1128919					963811							1194828					
HE8UY74 HAHIY08 H2CBH45 HMVAM09						Ť		HAHIY08	H2CBH45												HMVAM09					
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H0574: 1, H0013: 1, H0544: 1, H0023: 1, H0071: 1, H0286: 1, H0100: 1, H0494: 1, S0370: 1, L0770: 1, L0646: 1, L0764: 1, L0771: 1, L0363: 1, L0774: 1, L0659: 1, L07789: 1, L0666: 1, S0126: 1, H0522: 1, L0754: 1, L0747: 1 and L0754: 1, L0747: 1 and	1	AR061: 5, AR089: 2 S0010: 4, S0222: 3,	H0455: 2, L0803: 2,	L0439: 2, L0745: 2,	S0282: 1, S0400: 1,	H0456: 1, H0441: 1,	S0346: 1, H0509: 1,	L0769: 1, L0438: 1,	L0756: 1 and S0106: 1.				ı	•	AR089: 1, AR061: 1,	AR050: 0	
		Glu-62 to Tyr-67, Pro-169 to Lys-179,		χ,				His-393 to Ala-399,	Asp-420 to Asn-425,	Thr-460 to Lys-473,	Ser-488 to Gly-502.	GIU-62 to 1 yr-6/,	Ser-129 to Asp-135.	Leu-53 to Gln-58,	Phe-162 to Gly-167,	Gin-282 to Ala-287.	
	1106	816									1,01	/011		817			
·	2 - 802	96 - 1646									000	88 - 540		67 - 927			1
	508	218										506		219			
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		HFPEN04												HSLJD02	-		
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		AR089: 6, AR061: 2	H0250: 5, L0770: 2,	L0438: 2, L0439: 2,	L0754: 2, S0114: 1,	H0459: 1, H0489: 1,	S0278: 1, H0069: 1,	H0575: 1, H0318: 1,	H0123: 1, L0471: 1,	H0071: 1, H0328: 1,	H0634: 1, T0067: 1,	L0351: 1, H0560: 1,	S0142: 1, S0344: 1,	S0426: 1, L0763: 1,	L0769: 1, L0761: 1,	L0662: 1, L0363: 1,	L0364: 1, L0805: 1,	L0666: 1. L0664: 1.	S0126: 1, H0658: 1,	H0670: 1, H0521: 1,	H0522: 1, S0044: 1,	H0555: 1, H0576: 1,	L0748: 1 and L0755: 1.				AR089: 2, AR061: 1	L0754: 8, L0777: 8,
Leu-53 to Gln-58,	Phe-162 to Gly-167, Gln-282 to Ala-287.	Leu-31 to Gly-41,	Arg-137 to Ser-143,	Glu-241 to Glu-260.																				Leu-31 to Gly-41,	Arg-137 to Ser-143,	Glu-241 to Glu-260.	Ser-1 to Leu-13,	Pro-17 to Gly-31,
1108		818																						1109			819	
47 - 907		1637 - 819																						1637 - 819			140 - 1681	
510		220																	-					511			221	
965826	·, ——_	1220164																						966752			1217931	
		HDPFZ30														,						,					HPJCR33	
		210																									211	

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L0439: 5, H0266: 2, L0438: 2, H0672: 2, S0152: 2, L0745: 2, L0758: 2, H0650: 1, S0212: 1, S0045: 1, S0212: 1, S0045: 1, H056: 1, H0486: 1, H054: 1, H0671: 1, H0551: 1, H0269: 1, S0344: 1, L0794: 1, L0766: 1, L0803: 1, L0805: 1, L0659: 1, H0547: 1, H0519: 1, S0126: 1, H0711: 1, H0528: 1, S0028: 1, L0750: 1, L0780: 1, L0750: 1, L0780: 1, L0751: 1, S0192: 1, H0423: 1 and H0293: 1.		AR089: 1, AR061: 1 L0766: 2, H0264: 1 and H0521: 1.	1	AR050: 3, AR051: 1, AR089: 0, AR061: 0 H0013: 3, L0794: 2,	L0439: 2, L0756: 2,	S0001: 1, H0619: 1,
Thr-44 to Leu-54, His-84 to Arg-95, Asn-105 to Gln-116, Pro-132 to Leu-138, Glu-148 to Gly-157, Arg-180 to Trp-185, Asn-340 to Glu-346, Asn-401 to Cys-412, Asp-430 to Ala-435, Thr-473 to Lys-478, Pro-490 to Tyr-498.		Ser-10 to His-15.	Ser-67 to Trp-77.			
	1110	820	1111	821		
	1 - 375	784 - 599	918 - 1196	318 - 749		
	512	222	513	223		
	966758	1081321	008996	971296		
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L0638: 1, L0641: 1,	L0776: 1 and H0435: 1.	AR050: 193, AR054:	122, AR051: 84,	AR089: 0, AR061: 0	H0255: 59, H0254: 10,	H0617: 9, L0747: 8,	S0358: 7, H0486: 6,	L0655: 6, H0208: 4,	H0545: 4, H0024: 4,	S0354: 3, H0250: 3,	H0123: 3, H0031: 3,	L0659: 3, S0328: 3,	L0731: 3, H0583: 2,	L0808: 2, L0785: 2,	H0662: 2, H0586: 2,	H0618: 2, H0253: 2,	H0424: 2, H0264: 2,	H0488: 2, H0100: 2,	L0771: 2, L0806: 2,	L0809: 2, H0144: 2,	H0689: 2, L0749: 2,	L0750: 2, L0779: 2,	L0777: 2, H0707: 2,	L0595: 2, H0624: 1,	H0341: 1, S0356: 1,	S0360: 1, H0619: 1,	H0411: 1, H0370: 1,	H0485: 1, H0635: 1,	H0025: 1, H0108: 1,
		Gly-1 to Pro-7,	Gly-23 to Gly-50,	Ser-53 to Pro-84,	Ser-89 to Thr-129,	Gly-140 to Gly-145,	Pro-148 to Lys-158,	Thr-161 to Ser-167,	Leu-179 to Arg-189,	Pro-203 to Lys-211,	Glu-233 to Asp-240,	Lys-261 to Gly-288,	Arg-296 to Glu-305,	Ala-315 to Arg-353,	Glu-372 to Pro-382,	Gln-395 to Glu-408,	Asn-419 to Gly-427,	Ala-458 to Gly-463,	Pro-477 to Ala-483.										
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H0318: 1, H0581: 1, T0110: 1, H0231: 1, L0738: 1, H0086: 1, H0644: 1, H0181: 1, H0644: 1, H0181: 1, H0646: 1, L0371: 1, L0766: 1, L0764: 1, L0774: 1, L0803: 1, L0774: 1, L0657: 1, L0368: 1, L0787: 1, L0665: 1, H0519: 1, L0665: 1, H0696: 1, S0380: 1, H0696: 1, S0380: 1, H0696: 1, L0439: 1, L0780: 1, L0755: 1, H0445: 1 and L0755: 1, H0445: 1 and		AR089: 1, AR061: 0 L0659: 12, L0769: 10, L0666: 8, L0747: 8, L0759: 7, L0439: 6,
	Gln-1 to Ala-7, Thr-36 to Trp-42, Gly-45 to Gly-52, Glu-77 to Pro-89, Gly-105 to Gly-132, Ser-135 to Glu-162.	Arg-27 to Gly-40, Arg-67 to Asp-91.
	1112	823
	1121 - 2929	286 - 14
	514	225
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L0757: 6, L0756: 5,	L0770: 4, L0761: 4,	H0521: 4, L0/49: 4,	LU/50: 4, LU///. 4,	H0486: 3, H0544: 3,	H0623: 3, L0662: 3,	L0794: 3, L0766: 3,	L0774: 3, L0664: 3,	L0740: 3, L0779: 3,	H0423: 3, S0418: 2,	S0360: 2, L0717: 2,	H0549: 2, H0618: 2,	H0581: 2, H0545: 2,	H0510: 2, H0617: 2,	L0763: 2, L0772: 2,	L0642: 2, L0764: 2,	L0775: 2, L0655: 2,	L0789: 2, S0374: 2,	H0658: 2, H0522: 2,	H0631: 2, L0745: 2,	L0731: 2, H0556: 1,	T0049: 1, H0656: 1,	L0785: 1, H0483: 1,	H0661: 1, H0664: 1,	H0662: 1, S0420: 1,	S0354: 1, S0358: 1,	H0580: 1, S0468: 1,	S0132: 1, S0222: 1,	H0441: 1, H0586: 1,
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H0587: 1, H0497: 1, H0069: 1, H0427: 1, S0280: 1, H0046: 1, H0457: 1, H0081: 1, H0024: 1, T0010: 1,	H0594: 1, H0188: 1, H0687: 1, H0553: 1,	0124: 1, H0494: 1, 0641: 1, S0422: 1.	0002: 1, S0426: 1,	L0372: 1, L0646: 1,	L0374: 1, L0648: 1,	20649: 1, L0803: 1,	_0651: 1, L0653: 1,		 20783: 1, L0809: 1,	 		H0547: 1, H0689: 1,	H0690: 1, H0683: 1,	H0670: 1, S0378: 1,	S0152: 1, H0555: 1,	H0436: 1, S0392: 1,	L0742: 1, L0751: 1,	0780: 1, H0668: 1,	H0653: 1, S0242: 1,	H0542: 1, H0543: 1 and	S0460: 1.
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		: 23, AR061: 4,	_	L0741: 9,)777: 6,	0617: 5,	753: 4,	775: 3,	378: 3,	040: 2,	0046: 2,	0006: 2,	038: 2,	370: 2,	0670: 2,	747: 2,	342: 1,	030: 1,	0007: 1,)261: 1,	0441: 1,	0082: 1,	0010: 1)271: 1.	H0424: 1,	0181: 1,	144: 1,	520: 1,
,		AR054: 23,	AR089: 3,	L0439: 31, L0741: 9,	L0438: 7, L0777: 6,	H0052: 5, H0617: 5,	L0748: 4, L0753: 4,	L0769: 3, L0775: 3,	L0776: 3, S0378: 3,	L0779: 3, S0040: 2,	L0103: 2, H0046: 2,	H0284: 2, T0006: 2,	S0036: 2, S0038: 2,	L0351: 2, S0370: 2,	L0764: 2, H	L0602: 2, L0747: 2,	L0592: 2, S0342:	S0282: 1, S0030:	H0484: 1, S0007:	S0278: 1, H0261:	S0222: 1, H0441:	H0156: 1, T0082:	H0194: 1, T0010:	S6028: 1, H0271:	L0483: 1, H	H0213: 1, H0181:	S0112: 1, S0144:	S0002: 1, L0520: 1,
Pro-1 to Asn-14,	Lys-17 to Phe-23,	Gln-25 to Gly-33,	Pro-49 to Gly-55,	Gly-89 to Glu-97,	Ser-176 to Glu-183,	Thr-231 to Gly-240,	Pro-267 to Thr-275,	Pro-297 to Asp-308,	Asp-340 to Ser-345,	Arg-353 to Leu-361,	Pro-375 to Gly-382,	Glu-393 to Trp-410,	Gly-470 to Ser-475,	Fyr-504 to Arg-516,	Gly-531 to Thr-539,	Pro-571 to Gln-580,	Leu-591 to Glu-598,	Gln-601 to Gly-611,	Gly-649 to Ser-654,	Asp-661 to Leu-666,	Ala-669 to Glu-674.							
Pro-1	Lys-1	Gln-2	Pro-4	Gly-8	Ser-1	Thr-2	Pro-2	Pro-2	Asp-3	Arg-3	Pro-3	Glu-3	Gly-4	Tyr-5	Gly-5	Pro-5	Leu-5	Gln-6	Gly-6	Asp-(Ala-6							
1113		824																										
1 - 195		1 - 2037																										
515		226	_																									
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		HSXBV89																										
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L0762: 1, L0763: 1, L0638: 1, L0772: 1, L0768: 1, L0653: 1, L0659: 1, L0636: 1, L0367: 1, L0791: 1, L0665: 1, L0791: 1, H0672: 1, H0539: 1, S0032: 1, L0742: 1, L0740: 1, L0758: 1 and H0667: 1.	:	AR054: 189, AR051:	68, AR050: 35, AR089:				AR061: 3, AR089: 1 H0618: 3 and H0253: 1.				AR054: 334, AR050:	251, AR051: 249,	AR061: 6, AR089: 6	1 10/20: 14, 100004: 11
	Gln-20 to Gly-28, Pro-44 to Gly-50.	Leu-50 to Asp-61,	Ser-100 to Leu-107, Pro-119 to Leu-125	110-117 to Ecu-123.	Leu-50 to Asp-61,	Ser-100 to Leu-107, Ala-120 to Thr-130.	Tyr-52 to Gln-60.	Tyr-52 to Gln-60,	Phe-86 to Ala-94,	Lys-111 to Arg-118, His-193 to Tyr-198.	Val-2 to Cys-17,	Cys-41 to Gln-52,	Glu-70 to Phe-82,	014-07 to 001-71,
	1114	825			1115		826	1116			827			
	3 - 509	3 - 572			3 - 503		2 - 802	2 - 802			1 - 1302			
	516	227			517		228	518			229			
	971821	1143756			973131		1085651	973302			1207835			
		HBIOZ10					HTLEJ11				HAWAM69 1207835			
		217					218				219			

H0251: 9, L0731: 9, S0360: 5, H0013: 5,	L0659: 5, L0747: 5,	H0252: 4, H0328: 4,	L0666: 4, L0439: 4,	H0135: 3, L0764: 3,	L0783: 3, L0749: 3,	S0358: 2, L0776: 2,	L0663: 2, H0651: 2,	L0744: 2, L0754: 2,	H0675: 1, H0329: 1,	H0619: 1, L0717: 1,	H0369: 1, H0550: 1,	H0333: 1, H0632: 1,	H0486: 1, T0060: 1,	H0042: 1, H0575: 1,	H0618: 1, H0150: 1,	H0123: 1, H0050: 1,	H0105: 1, T0003: 1,	H0024: 1, H0510: 1,	H0594: 1, H0028: 1,	H0644: 1, S0364: 1,	S0366: 1, H0591: 1,	H0100: 1, L0763: 1,	L0631: 1, L0637: 1,	L0646: 1, L0641: 1,	L0644: 1, L0649: 1,	L0803: 1, L0775: 1,	 L0519: 1, L0793: 1,	L0665: 1, H0144: 1,
Lys-126 to Gly-132, Val-134 to Gly-145,	Glu-167 to Arg-180,	Glu-187 to Ser-200,	Cys-204 to Ser-210,	Glu-213 to Asp-221,	Thr-260 to Ala-273,	Ala-278 to Gln-290,	Ser-317 to His-333,	Leu-347 to Gly-356,	Lys-358 to Phe-363,	Leu-367 to Cys-376,	Asp-385 to Ser-391,	Glu-406 to Gly-434.	•						,									
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T 0128. 1 110601. 1	L0738. 1, R0034. 1, H0672: 1, S0380: 1, L0748: 1, L0759: 1, L0596: 1, L0366: 1, L0600: 1 and H0352: 1.						AR089: 1, AR061: 1	H0667: 1							AR089: 1, AR061: 0	H0521: 1			AR061: 3, AR089: 2	L0750: 2, H0024: 1,	H0039: 1, H0622: 1,	H0040: 1 and S0434: 1.	AR061: 1, AR089: 1	L0774: 2 and H0144:	- -
		Cys-38 to Gly-43, Glv-70 to Pro-82.	Arg-129 to Glu-134,	Gly-139 to Gly-144.	Leu-23 to Gly-32,	Lys-34 to Lys-40.	Ala-20 to Val-28,	Pro-60 to Cys-66,	Ser-118 to Asp-123,	Leu-225 to Asp-236,	Thr-267 to His-274.	Ala-6 to Ala-11,	Phe-19 to Asn-24,	Val-29 to Lys-34.	Arg-9 to Leu-17,	Pro-90 to Asn-95,	Lys-115 to Glu-125.		Asp-40 to Asn-49,	Cys-65 to Gly-71.			Phe-8 to Lys-27,	Ser-79 to Ser-87,	Cys-102 to Val-116.
		1117			11118		828					1119		;	829			1120	830				831		
		1010 - 1441			154 - 2		1238 - 2074					117 - 326			195 - 800			405 - 809	3 - 422	-			362 - 871		
		519			520		230					521		:	231			522	232				233		ļ
		943104			973465		1056288					973894			1027241			973945	974296				1079624		
							HSCKD11								HDPLT62				HTPFX16			!	990N63H		
							220								221				222				223		

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	AR061: 0, AR089: 0 S0045: 6, H0255: 5, S0028: 4, S0031: 2, S0260: 2, H0341: 1, S0278: 1, H0333: 1, H0271: 1, H0100: 1, S0216: 1, S0044: 1 and S0390: 1.		AR061: 3, AR089: 1 S0001: 1		AR061: 1, AR089: 1 H0581: 1, H0494: 1, H0521: 1, H0444: 1, H0543: 1 and L0465: 1.	AR061: 10, AR089: 4 L0754: 4, H0616: 1 and H0509: 1.
Phe-8 to Lys-27, Ser-79 to Ser-87, Cys-102 to Val-116.		Ala-324 to Phe-332, Arg-336 to Thr-343, Pro-373 to Arg-384,	Gln-16 to Gly-25, Thr-32 to Gly-42, Asn-46 to Asp-52.	Lys-1 to Arg-7, Phe-10 to Arg-19.		Phe-61 to Thr-68, Arg-70 to Ser-76, Gln-88 to Arg-93, Pro-145 to Gln-157, Glu-164 to Ser-171,
1121	832	1122	833	1123	834	835
362 - 871	218 - 1921	210 - 1847	1 - 435	3 - 272	1 - 186	3 - 662
523	234	524	235	525	236	237
974353	1154068	974784	1126294	578868	734565	1144557
	HSDJ144		HFXDP53		HWADY66	HLDBC63
	224		225		226	227

				AR061: 1, AR089: 1	H0013: 2, S0468: 1,	S0046: 1, H0592: 1,	H0266: 1, S3014: 1,	S0028: 1 and S0196: 1.						AR061: 25, AR089: 15	L0783: 3, S0007: 2,	L0782: 2, H0539: 2,	L0747: 2, H0333: 1,	H0253: 1, H0052: 1,	H0546: 1, T0006: 1,	H0135: 1, L0770: 1,	L0769: 1, L0776: 1,	L0745: 1, L0777: 1 and	L0753: 1.		L0783: 3, S0007: 2,	L0782: 2, H0539: 2,	L0747: 2, H0333: 1,	H0253: 1, H0052: 1,	H0546: 1, 10006: 1,
Gly-215 to Thr-220.	Phe-61 to Thr-68,	Arg-70 to Ser-76,	Gln-88 to Arg-93.	Arg-20 to Thr-27,	Leu-40 to Gly-45,	His-57 to Lys-74,	Thr-97 to Ser-112,	Asp-150 to Ser-155,	Leu-177 to Asp-182.	Thr-33 to Lys-47,	Thr-70 to Ser-85,	Asp-123 to Ser-128,	Leu-150 to Asp-155.																
	1124			836						1125				837										1126	838				
	3 - 416			3 - 665						82 - 663				3 - 698										3 - 422	3 - 428				
	526			238						527				239										528	240				
	745061			978211						752981				1181355				_						753093	753094				
				HFIVB68										HTLAC56			_					-			HSSAD41				
				228										229											230				

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H0135: 1, L0770: 1,	L0769: 1, L0776: 1,	L0745: 1, L0777: 1 and	L0753: 1.	AR061: 0, AR089: 0	L0157: 2, H0620: 2,	1.0666: 2. \$0001: 1.	L0717: 1, H0549: 1.	S0222: 1, H0581: 1,	H0194: 1, H0015: 1,	H0399: 1, H0271: 1,	H0688: 1, H0428: 1,	H0124: 1, L0637: 1,	H0672: 1, L0439: 1,	L0750: 1 and H0423: 1.			AR089: 25, AR061: 11	L0601: 5, H0266: 4,	S0222: 3, H0265: 2,	H0556: 2, H0575: 2,	H0052: 2, H0271: 2,	S0114: 1, S0134: 1,	S0420: 1, H0393: 1,	H0550: 1, H0497: 1,	H0318: 1, H0581: 1,	H0251: 1, T0115: 1,	H0014: 1, H0286: 1,	H0494: 1, H0561: 1,	L0766: 1, L0657: 1,
				Ser-4 to Arg-15,	Glu-20 to Arg-62,	Pro-107 to Glv-112.	Glv-128 to Glv-134.	Gln-137 to Arg-143,		Tyr-239 to Asn-247,			Ser-356 to Leu-361,		Glu-5 to Arg-15,	Glu-20 to Arg-62.	Asp-34 to Asp-49,	Gly-276 to Ala-286,		۶.									
				839											1127		840												
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				241											529		242					_							
	_			1218436											765375		1188787												
				HCFMT57													HDAAV61												
				231													232												

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H0698: 1, H0684: 1, S0330: 1, H0521: 1, S3014: 1, L0777: 1, S0260: 1, L0591: 1, L0594: 1 and H0543: 1.		AR089: 4, AR061: 0	H0521: 1, H0494: 1, H0521: 1, H0543: 1 and	L0465: 1.					AR061: 6, AR089: 3	H0038: 4, L0758: 3,	H0616: 2, L0794: 2,	L0747: 2, L0803: 1,	L0789: 1 and L0590: 1.		AR061: 2, AR089: 1	H0370: 2, S0002: 1,	S0428: 1 and S0027: 1.			-		AR089: 5, AR061: 4	S0328: 5, H0264: 4,	L0549: 3, S0306: 2,
	Asp-90 to Lys-105.	Gly-2 to Asp-11,	Ala-23 to Ash-30, Phe-48 to Glv-56.	Glu-99 to His-105,	Glu-187 to Glu-192.	Ala-13 to Asn-20,	Phe-38 to Gly-46,	Glu-89 to His-95.	Pro-27 to Ala-35,	Ser-138 to Asn-144.				Pro-27 to Ala-35.	Ala-3 to Arg-20,	Ser-33 to Asp-39,	Leu-70 to Ser-76,	Pro-117 to Tyr-122.	Ser-1 to Asp-7,	Leu-38 to Ser-44,	Pro-85 to Tyr-90.	Arg-32 to Asn-39,	Leu-76 to Gly-82,	Cys-112 to Ser-119,
	1128	841				1129			842					1130	843				1131			844		
	2 - 343	2 - 637				2 - 445			1 - 516					2 - 520	1 - 480				98 - 481			25 - 1029		
	530	243				531			244					532	245				533			246		ļ.
	810305	1096253				810824			1126312					815852	1121800				823869			1216498		
		HDPKD75							HTEON29						HSKAC24							HTJAA71		
		233							234						235							236		

H0379: 1, H0487: 1, S0448: 1, S0450: 1, L0648: 1, L0551: 1 and S0330: 1.	AR061: 2, AR089: 1 L0758: 14, H0038: 5, L0779: 4, L0794: 2 and H0616: 1.		AR061: 3, AR089: 1 H0144: 2 and S0053: 1	AR089: 1, AR061: 0 L0439: 12, L0748: 11, L0751: 11, L0769: 7,
Gly-129 to Gly-135, Ala-141 to Val-167, Ser-181 to Ile-194, Ser-201 to Gly-239, Ser-245 to Gln-250, Thr-256 to Thr-293, Ala-306 to Asp-335.	Pro-7 to Arg-12, Phe-32 to Ile-37, Arg-39 to Lys-45, Leu-47 to Gly-53, Lys-102 to Lys-108, Asp-117 to Gly-122.	Pro-9 to Arg-14, Phe-34 to Ile-39, Arg-41 to Lys-47, Leu-49 to Gly-55, Lys-104 to Lys-110, Asp-119 to Gly-124.	Glu-134 to Glu-144, Gln-151 to Arg-161, Arg-167 to Gly-172, Tyr-183 to Asn-188, Asn-193 to Phe-209, Asp-261 to Trp-272.	Glu-75 to Glu-86, Leu-176 to Gln-181, Ser-276 to Ala-282,
133	845	1133	846	1134
23. 334	2 - 562	3 - 569	3 - 863	2 - 328
534	247	535	248	249
846687	1124378	846714	1125192	856343 1202275
	HTEKS20		HE9TK49	856343 HCHAT01 1202275
	237		238	239

H0046: 6, L0756: 6, L0775: 5, L0666: 5,	L0747: 5, L0770: 4,	L0438: 4, L0740: 4,	L0777: 4, H0617: 3,	L0662: 3, L0774: 3,	L0776: 3, H0521: 3,	S0037: 3, L0749: 3,	L0731: 3, L0757: 3,	L0758: 3, S0212: 2,	S0222: 2, H0586: 2,	H0587: 2, H0333: 2,	H0156: 2, H0052: 2,	S0388: 2, H0290: 2,	L0640: 2, L0521: 2,	L0766: 2, L0375: 2,	L0659: 2, L0783: 2,	H0144: 2, H0539: 2,	L0755: 2, H0445: 2,	L0596: 2, L0599: 2,	H0149: 1, S0342: 1,	H0294: 1, S0114: 1,	H0484: 1, H0483: 1,	H0664: 1, H0638: 1,	S0418: 1, S0420: 1,	L0005: 1, S0046: 1,	S0300: 1, H0549: 1,	H0550: 1, H0370: 1,	H0497: 1, H0331: 1,	H0486: 1, H0575: 1,	S0010: 1, H0434: 1,
Leu-320 to Lys-325, Met-366 to Ser-373.	Leu-414 to Asp-419,	Thr-471 to His-506,	Lys-513 to Ile-522,	Pro-526 to Gln-532,	Asp-547 to Asp-552,	Ala-576 to Cys-585,	Glu-588 to His-598,	Gly-637 to Pro-645,	Leu-649 to Asp-657,	Ile-733 to Phe-743,	Ala-746 to Gly-753.																		
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H0327: 1, H0457: 1, H0041: 1, H0081: 1,	H0620: 1, H0024: 1, H0057: 1, H0051: 1,	H0083: 1, H0266: 1,	H0188: 1, S0250: 1,	H0685: 1, H0044: 1, H0674: 1, S0366: 1,	H0087: 1, H0116: 1,	H0488: 1, H0494: 1,	H0131: 1, S0150: 1,	H0633: 1, H0649: 1,	H0652: 1, L0369: 1,	L0638: 1, L0646: 1,	L0641: 1, L0771: 1,	L0773: 1, L0653: 1,	L0658: 1, L0809: 1,	L0789: 1, L0663: 1,	L0664: 1, H0693: 1,	H0520: 1, S0126: 1,	H0682: 1, H0659: 1,	S0330: 1, H0696: 1,	S0174: 1, H0555: 1,	S3012: 1, S0028: 1,	L0742: 1, L0744: 1,	L0745: 1, L0750: 1,	L0786: 1, L0779: 1,	L0752: 1, S0434: 1,	L0366: 1, H0542: 1,	H0423: 1 and H0352: 1.
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	R089: 6, AR061: 4, L0666: 6, L0761: 4, 10486: 3, L0794: 3, 0659: 3, H0255: 2, 0358: 2, H0052: 2, 0358: 2, H0692: 1, 0116: 1, H0581: 1, 10087: 1, L0763: 1, 0375: 1, L0655: 1, 0375: 1, L0655: 1, 0375: 1, L0655: 1, 0375: 1, H0672: 1, 0378: 1, H0672: 1, 0310: 1, H0672: 1, 0328: 1, H0539: 1 a 10436: 1.		AR061: 3, AR089: H0521: 7, H0580: 5, L0665: 4, H0457: 3,	745: 3, 306: 2,	′50: 2, 650: 1,
	AR089: 6, AR061: 4 L0666: 6, L0761: 4 H0486: 3, L0794: 3, L0659: 3, H0255: 2, S0358: 2, H0052: 2, L0809: 2, L0743: 2, L0759: 2, H0692: 1, S0116: 1, H0581: 1, H0597: 1, L0763: 1, L0764: 1, L0766: 1, L0775: 1, L0655: 1, L0788: 1, L0655: 1, S0310: 1, H0672: 1, S0328: 1, H0539: 1		AR061: 3, AR089: H0521: 7, H0580: 3, L0665: 4, H0457: 3,	3, L07 2, L08	L0789: 2, L0750: 2 H0542: 2, H0650: 1
	AR089: 6, AR061: L0666: 6, L0761: 4, H0486: 3, L0794: 3, L0659: 3, H0255: 2, S0358: 2, H0052: 2, L0809: 2, L0743: 2, L0759: 2, H0692: 1, S0116: 1, H0581: 1, H0087: 1, L0763: 1, L0764: 1, L0766: 1, L0764: 1, L0766: 1, L0764: 1, L0655: 1, L0768: 1, L0655: 1, S0310: 1, H0672: 1, S0328: 1, H0539: 1 an H0436: 1.		AR061 H052 L0665:	L0766: 3, L0745: 3, L0761: 2, L0806: 2,	L0789: H0542
6, 99, 117, -163.	0,	, 6	2, 2, 2,	_	
o Lys-6 to Ser-	Pro-14 o Arg-{ to Gln	Ala-10 o Ala-2	D Lys-2 D Phe-4 Gln-66	to Glu	!
Ser-20 to Ala-26, Leu-64 to Lys-69, Met-110 to Ser-117, Leu-158 to Asp-163	Pro-7 to Pro-14, Asp-70 to Arg-80, Asp-145 to Gln-152.	Ser-1 to Ala-10, Cys-23 to Ala-29	Pro-19 to Lys-29, His-38 to Phe-45, Ile-52 to Gln-66,	Glu-123 to Glu-138.	
1135	848	1136	849		
- 1556	- 664	619	- 673		
771 -	128 -	2 - (101		
537	250	538	251		
867209	1150867	878658	883382		
	HCEEN06		HDPKI83		
	240		241		·

H0656: 1, H0581: 1,	H0271: 1, H0553: 1,	H0413: 1, H0641: 1,	S0002: 1, L0774: 1,	H0660: 1, H0555: 1,	L0753: 1 and H0423: 1.	AR089: 2, AR061: 1	L0766: 19, L0439: 9,	L0803: 7, L0740: 7,	L0752: 7, L0770: 5,	L0659: 5, L0731: 5,	L0805: 4, L0777: 4,	H0657: 3, H0373: 3,	L0804: 3, S0152: 3,	L0748: 3, L0749: 3,	L0779: 3, H0650: 2,	L0471: 2, S6028: 2,	H0032: 2, L0783: 2,	L0438: 2, H0521: 2,	H0478: 2, L0744: 2,	L0747: 2, L0750: 2,	L0485: 2, S0424: 2,	S0134: 1, S0354: 1,	S0358: 1, H0580: 1,	S0222: 1, H0013: 1,	L0021: 1, H0575: 1,	H0050: 1, H0014: 1,	H0051: 1, H0031: 1,	H0553: 1, H0165: 1,	JH0551: 1, H0509: 1,
						His-4 to Gly-21,	Thr-55 to Ser-66,		Thr-168 to Ser-174.									-											
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H0132: 1, H0652: 1, S0002: 1, H0529: 1, L0763: 1, L0772: 1, L0372: 1, L0771: 1, L0521: 1, L0662: 1, L0768: 1, L0386: 1, L0778: 1, L0774: 1, L0778: 1, L0655: 1, L0778: 1, L0789: 1, L0782: 1, L0789: 1, H0144: 1, L0352: 1, H0659: 1, H0672: 1, S0378: 1, S0380: 1, S0378: 1, S0380: 1, L0757: 1, L0758: 1 and H0543: 1.	AR054: 2, AR051: 1, AR089: 1, AR061: 0 H0642: 1	AR054: 60, AR051: 40, AR050: 36, AR089: 5, AR061: 2 H0521: 4, H0486: 2, S0002: 2, L0770: 2, L0769: 2, L0766: 2, L0518: 2, L0783: 2,
	Gly-1 to Cys-7.	Ser-60 to Thr-71, Thr-82 to Leu-94, Gln-113 to Asp-123, Val-125 to Tyr-133, Leu-144 to Gly-149.
1137	851	852
91 - 1287	· [•	1 - 555
530	253	254
884004	886915	886936
\	HPCID78	HDTKQ14
	243	244

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, L0731: 2, H0556: 1, H0650: 1, H0488: 1, L0662: 1, L0655: 1, S0053: 1, L0759: 1 an	AR089: 3, AR061: 2 L0803: 4, L0758: 3, S0212: 2, S0358: 2, H0038: 2, L0770: 2, L0767: 2, L0766: 2, L0748: 2, L0751: 2, L0747: 2, L0759: 2, H0411: 1, H0392: 1, H0333: 1, L0021: 1, H0118: 1, T0115: 1, L0764: 1, L0769: 1, L0764: 1, L0775: 1, L0805: 1, L0806: 1, L0805: 1, L0806: 1, L0787: 1, H0547: 1, S0122: 1, H0555: 1,
·	Gln-15 to Gln-21.
	853
	1 - 471
	255
	888037
	HRACK83
	245

L0740: 1, L0749: 1, L0750: 1, L0755: 1 and L0595: 1.	AR089: 1, AR061: 0 S0354: 3, S0358: 3, H0587: 3, L0764: 3, L0803: 3, L0758: 3, H0036: 2, L0794: 2, L0809: 2, S0374: 2, S0376: 1, S0444: 1, S0408: 1, H0231: 1, L0783: 1, L0777: 1 and L0759: 1.		AR089: 2, AR061: 2 H0581: 3, H0622: 3, H0575: 2, H0090: 2, L0777: 2, L0757: 2, S0114: 1, H0650: 1, H0255: 1, S0360: 1, S0278: 1, H0486: 1, H0318: 1, H0046: 1, H0457: 1, H0039: 1, H0553: 1, L0763: 1,
	Met-15 to Ser-20, Asp-27 to Phe-37, Asp-53 to Tyr-59, Pro-86 to Asp-93, Pro-106 to Lys-129, Leu-139 to Ser-146, Thr-174 to Asp-183.	Asp-24 to Phe-34, Asp-50 to Tyr-56, Pro-83 to Asp-90, Pro-103 to Lys-126, Leu-136 to Ser-143, Thr-171 to Asp-180.	Val-14 to Lys-21, Gln-41 to Trp-46, Ala-98 to Pro-103.
	854	1138	855
	2 - 631	2 - 622	1 - 339
	256	540	257
	1156438	889498	894404
	HSIAO78		HWAGS73
	246		247

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	104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 152445, 152445, 152445, 152445, 152445, 152445, 152445, 174000, 179755, 182860, 182860, 191315, 230800, 266200, 600897, 601105, 601412, 601412,	
L0789: 1, H0144: 1, S0374: 1, S0310: 1, H0555: 1, L0758: 1, H0445: 1 and S0276: 1.	AR051: 86, AR054: 73, AR050: 67, AR089: 10, AR061: 5 H0706: 8, S0366: 5, S0364: 4, L0485: 4, L0604: 4, L0777: 3, L0623: 2, S0362: 2, H0373: 2, L0520: 2, L0747: 2, H0624: 1, H0619: 1, H0550: 1, H0619: 1, L0646: 1, L0809: 1, H0693: 1, S0328: 1 and H0214: 1.	
) C C E E	32, 50, 32, 07, 17.	Lys-59 to His-65, Pro-115 to Glu-121, Glu-130 to Ser-143,
	1221 856	- 569 1139
	258 1-1	541 1372
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		11, AR	5, AR(0	5, S022	7990H	S0260	S0282	S0046	, H019	H0268	S0027	L0747	, L075	, L060 ²	, H017	S0029	H061	, L0717	, H044	, H039	, S001	, H030	, S025(, H055	, S036	H0433: 1, H0269:
		AR051: 11, AR050:	AR054: 5, AR089:	१०६1:	H0031: 5, S0222: 4,	S0028: 4, H0662: 3,	748: 3,	276: 3,	S0360: 2, S0046: 2,	575: 2	S0036: 2, H0268: 2,	662: 2	754: 2	749: 2	777:2	595: 2	S0030: 1, S0029: 1,	358: 1	300: 1	0550: 1	H0431: 1, H0392:	[0060: 1, S0010:	0052: 1	S6028: 1, S0250: 1,	0252: 1	S0364: 1, S0366: 1,	0433: 1
	, ,	AR	A.	AF	<u> </u>	<u>S</u>	<u> </u>	<u>8</u>	<u>S</u>	H	S ₀	<u> </u>	<u>1</u>	<u> </u>	<u> </u>	<u>1</u>	<u>S</u>	<u>8</u>	S	Ħ	H	<u> </u>	Ħ	8	Ĕ	<u>S</u>	Ξ
Glu-163 to Gly-168, Asp-181 to Asp-187,	Asp-234 to Ser-241, Ile-257 to Asp-268.	-29,	/s-52,	al-112.																							
63 to (81 to 4	34 to 97	Thr-7 to Phe-29,	Thr-37 to Lys-52,	Glu-89 to Val-112.																							
Glu-1 Asp-1	Asp-2	Thr-7	Thr-3	Glu-8								_															
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COTECTION TO TENDE

H0412: 1, L0372: 1, L0804: 1, L0789: 1, L0666: 1, L0663: 1, S0126: 1, S0044: 1, H0345: 1, S0390: 1, S0037: 1, S3014: 1, L0743: 1, L0439: 1, L0750: 1, L0779: 1, L0599: 1, L0593: 1, L0366: 1 and H0653: 1.		AR089: 1, AR061: 0	H0341: 1, H0013: 1 and S0044: 1.										AR089: 1, AR061: 0	S0040: 1, H0250: 1,	T0048: 1, L0761: 1,	L0764: 1, L0783: 1,	L0809: 1, L0789: 1 and
	Thr-7 to Phe-29, Thr-37 to Lys-52, Glu-89 to Val-112	Gly-1 to Trp-7,	Leu-11 to Fne-21, Glu-46 to His-52,	Val-59 to Leu-73,	Tyr-79 to Cys-91,	His-111 to Tyr-117,	Ser-133 to Lys-149,	His-167 to Tyr-173,	His-195 to Tyr-201,	His-251 to Lys-25/.	Cys-36 to Asn-43,	Gln-74 to Trp-79.	Ser-2 to Gln-12,	Cys-14 to Met-19,	Ser-34 to Leu-41,	Pro-43 to Leu-48,	Glu-89 to Asp-111,
	1140	858									1141		859				
	404 - 2566	397 - 1167			,						149 - 466		3 - 404				
	542	260									543		261				
	908437	1128033				_					908549		1153909				
		HPWAY10											HOUDH19				
		250											251				

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L0757: 1.			AR089: 4, AR061: 1	H0171: 5, S0026: 3,	S0400: 2, L0471: 2,	H0031: 2, H0553: 2,	H0547: 2, H0521: 2,	L0759: 2, H0423: 2,	H0170: 1, H0583: 1,	H0656: 1, S0001: 1,	S0358: 1, S0360: 1,	H0244: 1, H0349: 1,	H0590: 1, H0310: 1,	H0014: 1, H0039: 1,	S0366: 1, H0551: 1,	L0351: 1, H0509: 1,	S0150: 1, L0369: 1,	L0796: 1, L0773: 1,	L0662: 1, L0766: 1,	L0803: 1, L0635: 1,	L0540: 1, H0519: 1,	H0684: 1, H0660: 1,	H0666: 1, S0044: 1,	H0478: 1, H0479: 1,	H0626: 1, L0748: 1,	L0740: 1, L0777: 1,	L0752: 1, L0755: 1 and	H0543: 1.
Ile-125 to Lys-134.	Thr-8 to Gln-19, Lys-26 to Glu-33,	Lys-41 to Ile-50.		Glu-72 to Pro-77,	Asp-91 to Pro-113,	Gln-124 to Asn-134,	Ser-182 to Ile-190,	Glu-215 to Gly-220,				His-301 to Lys-308,	_		Thr-358 to Tyr-363,	His-385 to Asn-398.												
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	52 - 573		124 - 1317																									
	544		262																									
	885806		1194719																									
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	AR089: 5, AR061: 2 S0358: 5, L0596: 3,	L0771: 2, L0758: 2,	S0354: 1, S03/6: 1, T0109: 1 H0036: 1	H0590: 1, L0040: 1,	H0038: 1, H0616: 1,	L0646: 1, L0764: 1,	L0768: 1, L0775: 1,	L0659: 1 and S0404: 1.			AR089: 2, AR061: 2	S0358: 6, L0794: 4,	L0758: 4, S0354: 3,	L0779: 3, L0596: 3,	S0376: 2, H0036: 2,	H0620: 2, H0063: 2,	L0771: 2, L0803: 2,	L0654: 2, L0659: 2,	T0109: 1, H0013: 1,	H0590: 1, H0052: 1,	H0596: 1, T0110: 1,	L0040: 1, H0090: 1,	H0038: 1, H0040: 1,	H0616: 1, H0429: 1,	H0561: 1, L0646: 1,	L0764: 1, L0768: 1,	L0766: 1, L0775: 1,
	Glu-20 to Gly-25, Gln-36 to Ser-48,	Ser-56 to Val-62.							Ser-25 to Ala-52,	Phe-64 to Glu-71.	Pro-17 to Ala-41,		Glu-84 to Gly-89,	2,	Ser-120 to Val-126.												
1143	861								1144		862																
104 - 460	589 - 951								134 - 535		3 - 557																
545	263								546		264																
909232	1152278			<u>.</u>	· -				909682		1152283																
	HWLFH94										HWMBM13 1152283		_														
	253										254																

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L0790: 1, L0792: 1, S0404: 1, S0390: 1, L0777: 1, L0755: 1, L0592: 1 and S0458: 1.						AR089: 1, AR061: 1	L0748: 5, S0242: 3,	H0615: 2, S0376: 1,	S0360: 1, L0717: 1,	L0641: 1, L0766: 1,	L0664: 1, H0478: 1,	L0593: 1 and S0196: 1.	r		AR061: 3, AR089: 2	L0750: 4, H0519: 3,	L0666: 2, L0565: 2,	H0539: 2, L0742: 2,	L0744: 2, L0754: 2,	L0777: 2, L0759: 2,	H0662: 1, S0045: 1,	S0346: 1, H0251: 1,	H0030: 1, H0628: 1,	H0674: 1, H0529: 1,	L0770: 1, L0764: 1,	L0526: 1, L0783: 1,
	Pro-11 to Ala-35,	Phe-47 to Glu-54,	Glu-78 to Gly-83,	Gln-94 to Ser-106,	Ser-114 to Val-120.	His-22 to Ile-35,	Phe-39 to Glu-47,			Met-93 to Ser-98.			Cys-1 to Val-10,	Ala-14 to Met-22.	Leu-6 to Tyr-15,	Ser-48 to Phe-53,	Asn-66 to Ser-71,		<u>_</u> ^	Arg-203 to Asp-212.						and the state of t
	1145		•			863							1146		864											
	3 - 539			-		79 - 1290							2 - 775		1 - 957											
	547					265							548		266											
	89606					1172525							857606		1182313											
						HFIUE75									HNTCP13											
						255									256						_					

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L0787: 1, H0547: 1, H0521: 1, H0696: 1, H0555: 1, L0747: 1, L0749: 1, L0786: 1, L0779: 1, L0780: 1, L0752: 1 and L0592: 1.	AR089: 1, AR061: 0 L0438: 6, L0751: 6, L0439: 5, L0770: 4, H0052: 2, H0620: 2, H0521: 2, L0756: 2, L0731: 2, L0758: 2, L0731: 2, L0758: 2, L0731: 1, H0662: 1, H0402: 1, S0418: 1, T0008: 1, S0418: 1, T0008: 1, S0222: 1, H0392: 1, H0581: 1, L0021: 1, H0581: 1, L0772: 1, L0766: 1, L0772: 1, L0766: 1, L0776: 1, L0559: 1, L0776: 1, L0522: 1, S0027: 1, H0522: 1,		AR089: 82, AR061: 18 H0580: 1	
	Gly-35 to Asp-41, Phe-113 to Met-119, Pro-164 to Glu-170, Val-173 to Gly-178, Met-180 to Glu-190, Thr-192 to Gln-199, His-206 to Glu-211, Arg-244 to Ile-257.		Leu-42 to Ile-47.	Trp-46 to Lys-51,
1147		1148	998	1149
1 - 960	3 - 824	2 - 577	439 - 161	55 - 696
549	267	550	268	551
07770	1175111	909782	1169125	862606
	нвівQ89		HWBEG18	
	257		258	

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	JR089: 1, AR061:	769: 4.	356: 3,	794: 3,	749: 3,	759: 3,	486: 2	805: 2,	789: 2,	485: 2,	H0556: 1, H0657: 1,	580: 1	261: 1	1455: 1	586: 1	635: 1	l, H0544: 1	050: 1	1288: 1	314: 1,	688: 1	366: 1,	063: 1	551: 1	S0002: 1	1, L0771: 1,	766: 1,
): 1, 1	110040. 34, L0/31 20534: 4. L0769: 4.	: 4, S0	: 3, L0	: 3, LO	: 3, L0	: 2, H0	: 2, L0	: 2, L0	: 2, L0	i. 1, H(H0637: 1, H0580:	: 1, H(): 1, H(): 1, H(: 1, H(3: 1, H(): 1, H(): 1, H(S0312: 1, S0314: 1	:: 1, H(H0644: 1, S0366:	i: 1, H(H0087: 1, H0551:	I. 1, S0	1, 1, 10	0648: 1, L0766:
	AR089:	L0534	H0521	L0800: 3, L0794: 3,	L0439	L0752	L0562	L0803	L0809	L0744	H0556: 1	H0637	H0208	H0609: 1, H0455: 1	H0600: 1, H0586: 1	H0331	H0618:	H0009: 1, H0050: 1	H0620	S0312	H0252	H064	H0135	H0087	H0264: 1,	L0639: 1	L0648
n-123, y-165.				•																							
9 to Asi 6 to Gl																						•					
Pro-109 to Asn-123, Phe-156 to Gly-165.																											
	298																										
	2174																										
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	269																										
	1221956												-		2												
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		126650,	126650,	154276,	173360,	173360,	180105,	222800,	246900,	602136,	602136,	602136,	602447					-	•				
		7q22-q31.1														,							
L0650: 1, L0378: 1, L0655: 1, H0699: 1, H0660: 1, L0743: 1, L0750: 1, L0777: 1, L0758: 1, L0097: 1, S0194: 1 and H0543: 1.		AR061: 0, AR089: 0	H0046: 34, L0731: 5, 0534: 4 1 0769: 4	70521: 4, S0356: 3,	L0800: 3, L0794: 3,	L0439: 3, L0749: 3,	L0752: 3, L0759: 3,	L0562: 2, H0486: 2,	L0803: 2, L0805: 2,	L0809: 2, L0789: 2,	L0744: 2, L0485: 2,	H0556: 1, H0657: 1,	H0637: 1, H0580: 1,	H0208: 1, H0261: 1,	H0609: 1, H0455: 1,	H0600: 1, H0586: 1,	H0331: 1, H0635: 1,	H0618: 1, H0544: 1,	H0009: 1, H0050: 1,	H0620: 1, H0288: 1,	S0312: 1, S0314: 1,	H0252: 1, H0688: 1,	H0644: 1, S0366: 1,
	Gln-8 to Glu-13.	7	!=	1.																			
	1150	898																•		_			
	18 - 914	46 - 228																					
	552	270																					
	909845	909846		-																			
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		260																					

H0135: 1, H0063: 1, H0087: 1, H0551: 1, H0264: 1, S0002: 1, L0639: 1, L0771: 1, L0650: 1, L0378: 1, L0655: 1, H0699: 1, H0660: 1, L0743: 1, L0750: 1, L0777: 1, L0758: 1, L0097: 1,	AR061: 8, AR089: 3 S0222: 1, H0052: 1,	H0194: 1, H0290: 1 and	H0264: 1.			AR061: 1, AR089: 1 H0009: 1					AR089: 9, AR061: 4	H0229: 1, H0590: 1,	S0049: 1, H0014: 1,	H0560: 1, L0439: 1 and H0543: 1.
	Arg-1 to Pro-15, Asn-17 to Leu-25,	Glu-27 to Pro-36,	Pro-41 to Pro-55,	Giu-58 to Gin-79.	ASII-0 to Pro-13.	Thr-37 to Ser-42, Gln-48 to Pro-55,	Ser-75 to Ala-80, Ser-95 to Val-111,	Gln-113 to Gly-124,	Glu-153 to Gly-161, Tyr-188 to Asp-193.	, , , , , , , , , , , , , , , , , , ,	Glu-20 to Val-26.			
	698			1151	1131	870				1152	871			
	2 - 550			2 202	2 - 372	112 - 753				209 - 565	3 - 317			
	271			553	CCC	272				554	273			
	1124531			000037	702207	1204971				910073	910074			
	нсенезз					HFCBB56					HAMFL82			
	261					262					263			

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AR061: 2, AR089: 1 L0439: 6, S0038: 3, L0803: 3, H0455: 2, L0769: 2, L0809: 2, L0741: 2, L0756: 2, S6024: 1, S0001: 1, H0663: 1, S0222: 1, H0441: 1, H0438: 1, H0036: 1, S0049: 1	L0774: 1, L0790: 1,	L0748: 1, L0749: 1,	H0707: 1, L0595: 1 and		AR050: 9, AR061: 2,	AR054: 2, AR089: 2,	AR051: 2	L0754: 14, L0777: 13,	H0553: 10, L0600: 7,	L0748: 6, L0803: 4,	L0749: 4, UNKWN: 4,	H0624: 3, S0280: 3,	S0126: 3, L0747: 3,
				Val-36 to Glu-43, Lys-66 to Glu-71		→ `		Thr-109 to Asp-115,	Cys-124 to Ile-130,	Cys-164 to Trp-169,	Thr-193 to Asp-207,	Thr-215 to Tyr-220,	Thr-228 to Ser-240,
872				1153	873								
402 - 1349				402 - 1535	2 - 3418								
274 40	 			555 40	275								
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264					265								_

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S0282: 2, H0024: 2,	H0030: 2, H0031: 2,	H0040: 2, L0438: 2,	, L0743: 2,	L0596: 2, L0603: 2,	S0212: 1, H0270: 1,	, H0427: 1	H0251: 1, H0309: 1	, S0340: 1,	S0250: 1, H0252: 1	, L0143: 1	H0038: 1, L0659: 1	.0565: 1, H0593: 1	H0684: 1, H0518: 1,	S0390: 1, S0260: 1 and															
S0282: 2,	H0030: 2	H0040: 2	S0028: 2,	L0596: 2	S0212: 1	H0244: 1	H0251: 1	S0338: 1, S0340:	S0250: 1	H0039: 1	H0038: 1	L0565: 1	H0684: 1	S0390: 1	H0506: 1					<u>_</u> .	Γ								
Ser-276,	Ala-334,	Asp-392,	Asn-428,	Ser-566,	Gly-623,	Ser-631,	Val-653,	Pro-681,	Glu-740,	.ys-748,	Cys-804,	Val-848,	Gly-857,	Gly-886,	Trp-913,	Thr-975,	o Ser-1057	Cys-1099	Cys-1120	o Phe-1139	0-15,	rp-54,	he-96,	Asp-115,	Ile-130,	Trp-169,	Asp-207,	Tyr-220,	Ser-240,
Glu-269 to Ser-276,	Glu-327 to Ala-334,	Asn-376 to Asp-392,	Gln-420 to Asn-428,	Tyr-547 to Ser-566,	Ala-616 to Gly-623,	Pro-625 to Ser-631,	Ser-647 to Val-653,	Gly-676 to Pro-681,	Tyr-720 to Glu-740,	Ile-742 to Lys-748,	Asp-792 to Cys-804,	Leu-841 to Val-848,	Gln-850 to Gly-857,	Asp-879 to Gly-886,	His-906 to Trp-913,	Pro-968 to Thr-975,	Gln-1051 to Ser-1057,	Pro-1092 to Cys-1099,	Lys-1113 to Cys-1120,	Trp-1126 to Phe-1139	Pro-9 to Pro-15,	Gly-49 to Trp-54,	Ser-91 to Phe-96,	Thr-109 to Asp-115,	Cys-124 to Ile-130,	Cys-164 to Trp-169,	Thr-193 to Asp-207,	Thr-215 to Tyr-220,	Thr-228 to Ser-240,
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			AR061: 7, AR089: 4	H0100: 1 and H0521:											AR089: 2, AR061: 1	L0794: 6, L0598: 2.	L0803: 2, L0748: 2,	S0040·1 S0046·1	H0431: 1, H0318: 1.	L0766: 1, L0606: 1,	L0749: 1, L0758: 1 and	S0192: 1.		AR061: 3, AR089: 2	L0766: 18, L0748: 11,	L0439: 9, L0749: 8,	L0438: 5, L0750: 5, L0777: 4, L0759: 4,	
Glu-269 to Ser-276,	Glu-327 to Ala-334,	Asn-3/6 to Asp-392, Gln-420 to Asn-428.	Gln-13 to Ser-18,	Glu-32 to Gly-37,	Ala-44 to Trp-49,	Glu-56 to Val-61,	Gln-68 to Lys-74,	Ala-83 to Glu-88,	Arg-111 to Gly-117,	Tyr-123 to His-143,	Ser-167 to Met-201.	Gln-13 to Ser-18,	77 -10 -10 -10	Glu-32 to Gly-37, Ala-44 to Tro-49.	Thr-70 to Ala-83,	Glv-105 to Asn-110,	Ser-181 to Val-187.						Lys-27 to Ile-43.	Arg-24 to Arg-30,	Arg-39 to Tyr-44,	Lys-78 to Glu-91,	Val-215 to Lys-223.	
			874		•					-		1155			875								1156	9/8				
			1 - 612									1 - 264			853 - 1563								160 - 846	415 - 1530				
		-	276									557			277								558	278				
			1153883									911263			1162680		_						911293	1197460				
			HE6GF02												HOUFT36					-				HAGGF84				_
			266												267									268				_

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H0441: 3, H0052: 3, I: 0637: 3, I:0761: 3.	L0740: 3, L0747: 3,	L0103: 2, H0574: 2,	H0156: 2, H0597: 2,	S0250: 2, L0649: 2,	L0803: 2, L0806: 2,	L0792: 2, S3014: 2,	L0757: 2, L0485: 2,	L0599: 2, H0171: 1,	S6024: 1, L0002: 1,	H0657: 1, H0341: 1,	S0358: 1, S0360: 1,	S0132: 1, L0717: 1,	H0632: 1, H0013: 1,	H0599: 1, S0010: 1,	S0346: 1, H0318: 1,	H0251: 1, T0115: 1,	H0544: 1, L0471: 1,	H0014: 1, S0362: 1,	H0083: 1, H0188: 1,	H0428: 1, H0646: 1,	H0538: 1, L0598: 1,	L0762: 1, L0763: 1,	L0769: 1, L0662: 1,	L0768: 1, L0776: 1,	L0655: 1, L0659: 1,	L0526: 1, L0783: 1,	L0789: 1, L0665: 1,	S0148: 1, H0520: 1,	H0519: 1, S0330: 1.

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L0602: 1, S0152: 1, S0136: 1, S0350: 1, L0752: 1, H0343: 1, L0366: 1, S0011: 1, H0665: 1, S0196: 1, H0423: 1, L0697: 1 and S0462: 1.		AR089: 1, AR061: 1 H0634: 2			AR061: 16, AR089: 6 L0804: 1, S0052: 1, H0144: 1 and H0659: 1.		AR089: 1, AR061: 0 L0750: 3, H0650: 2,	H0637: 2, H0265: 1, H0556: 1, S0222: 1.	0040: 1, H0280: 1,	20655: 1, L0789: 1 and 20666: 1.		AR089: 1, AR061: 0	L0439: 7, L0770: 4,)771: 4, L0779: 4,	H0688: 3, H0617: 2, L0533: 2, L0803: 2,
	Lys-14 to Glu-27.	<u> </u>	GIU-150 to Alg-15/.	Thr-15 to Asp-25, Glu-69 to Leu-89.	A I H		Gln-49 to Thr-69, A	茁 革	<u>H</u>	<u> </u>				Arg-75 to Gly-82, L(Thr-115 to Thr-120, H Leu-215 to Gly-222, L(
	1157	877		1158	878	1159	879				1160	880			
	1 - 333	2 - 571		2 - 337	718 - 212	1 - 564	788 - 1255			!	3 - 293	1 - 819			
	559	279		260	280	561	281				562	282			
	911312	1119031		911390	1171014	911476	1162674				911498	1228123			
		HTTKP07			HE9SE62		HUJAD24					HWLFG75			
		269			270		271					272			

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L0807: 2, L0791: 2, L0666: 2, H0539: 2, H0624: 1, S0400: 1, H0125: 1, H0192: 1, S0356: 1, S0354: 1, S0376: 1, S0360: 1, S0278: 1, H0550: 1, H0205: 1, S0049: 1, L0142: 1, L0455: 1, L0769: 1, L0794: 1, L0518: 1, L0809: 1, L0658: 1, H0689: 1, L0663: 1, H0689: 1, S0332: 1, H0214: 1, S0332: 1, L0747: 1, L0749: 1, L0758: 1,		AR061: 8, AR089: 3 L0758: 3, H0159: 2, S0001: 1, H0618: 1, H0660: 1 and L0779: 1	
Ser-230 to Trp-235, Pro-237 to Ala-248.	Val-10 to Gly-21, Pro-38 to Ala-59, Arg-70 to Gly-77, Thr-110 to Thr-115, Leu-210 to Gly-217, Ser-225 to Trp-230, Pro-232 to Arg-239.		Glu-1 to Ala-15,
	1161	881	1162
	1 - 750	9 - 785	1 - 381
	563	283	564
	916563	1092417	921593
		HT3BG12	
		273	

	AR061: 7, AR089: 5 H0618: 12, H0253: 8, H0038: 6, L0758: 6, L0779: 5, H0616: 3, T0041: 1, L0776: 1, S0274: 1 and H0543: 1.	AR089: 1, AR061: 1 H0670: 1	
Lys-25 to Ser-32, Asp-45 to Thr-51, Pro-59 to Pro-65, Pro-78 to Ser-85.	36, 36, 171, 171, 122, 157.	Gln-22 to Asp-41, Pro-49 to Thr-58, Leu-99 to Gly-107, Ala-117 to Ala-122, Gln-128 to Trp-134, Pro-136 to Pro-144, Phe-147 to Glu-153, Glu-183 to Val-188, Glu-195 to Glu-200, Glu-257 to Leu-265, Met-275 to Ser-283.	Gln-19 to Asp-38, Pro-46 to Thr-55, Leu-96 to Gly-104, Ala-114 to Ala-119, Gln-125 to Trp-131, Pro-133 to Pro-141,
	882	883	1163
	3 - 1355	2 - 850	1 - 840
	284	285	565
	922923	1194701	925952
	HTLJC71	НСОММ05	
	274	275	

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	AR061: 0, AR089: (S0036: 1, H0521: 1, H0436: 1 and S0390: 1		AR089: 33, AR061:	AR089: 4, AR061: 2 H0415: 13, H0414: 2, H0355: 1, H0517: 1 and H0539: 1.	AR061: 2, AR089: H0656: 2, S0360: 2, H0657: 1, H0662: 1, S0420: 1, S0356: 1, S0358: 1, S0132: 1, H0144: 1, H0520: 1, H0659: 1, H0658: 1, H0660: 1, H0672: 1,
	0, A 1, H0 1 and		: 33, A	5: 13, F 11, H00: 1.	AR061: 2, AR089 H0656: 2, S0360: H0657: 1, H0662: S0420: 1, S0356: 1 S0358: 1, S0132: 1 H0392: 1, S0022: H0144: 1, H0520: H0659: 1, H0658: H0660: 1, H0672:
	AR061 S0036 H0436:		AR089	AR089: H0415: H0355: 1, H0539: 1.	AR061: 2, AR089: H0656: 2, S0360: 2 H0657: 1, H0662: 1, S0420: 1, S0356: 1, S0358: 1, S0132: 1, H0392: 1, S0022: 1, H0144: 1, H0520: 1 H0659: 1, H0658: 1
.150, .185, .197, .262, .280.	.0, .0, .0, -219, -241, 272,	4, 19.	46.		
to Glu to Val to Glu to Leu to Ser	o Val-3 o Arg- o Ser-6 to Leu to Glu to Tyr-	Gly-7, o His-3 to Lys-4	o Asn-		to His-2
Phe-144 to Glu-150, Glu-180 to Val-185, Glu-192 to Glu-197, Glu-254 to Leu-262, Met-272 to Ser-280.	Ala-17 to Val-30, Thr-32 to Arg-39, Arg-55 to Ser-60, Ala-213 to Leu-219, Glu-236 to Glu-241, Ser-262 to Tyr-272, Pro-299 to Asn-305.	Arg-1 to Gly-7, Pro-25 to His-34, Leu-36 to Lys-49.	Lys-35 to Asn-46.		Lys-15 to Gly-23, Glu-36 to His-47.
	884	1164	885	886	887
	- 1654	731	- 483	. 320	981
	- 059	3-,	16 -	3-	,
	286	999	287	288	289
	1229928	926924	927411	928365	1179767
	HSLJE54		HTGED07	HOFNH30	HWNCY05 1179767
	276		277	278	279

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																						,				3q21-q25
S0380: 1, L0602: 1, H0653: 1 and H0677: 1.						AR089: 11, AR061: 3	H0521: 7, H0581: 3,	H0422: 3, H0650: 2,	H0486: 2, S0002: 2,	L0770: 2, L0769: 2,	L0766: 2, L0518: 2,	L0783: 2, L0777: 2,	L0731: 2, H0445: 2,	H0556: 1, H0583: 1,	H0657: 1, H0656: 1,	H0341: 1, H0575: 1,	H0457: 1, H0179: 1,	H0271: 1, L0055: 1,	H0264: 1, H0488: 1,	S0426: 1, L0662: 1,	L0775: 1, L0655: 1,	L0665: 1, S0053: 1,	_		i	AR089: 1, AR061: 1
	Lys-11 to Gly-19,	Glu-32 to His-43,	(Lys-00 to dia-00,	Pro-86 to Lys-98,	Lys-118 to Leu-128, Thr-142 to Tm-148.	Arg-17 to Leu-34,	Asp-44 to Ser-51,	Asp-63 to Gly-72,	Pro-74 to Gly-83,	Thr-97 to Met-102.						-										His-9 to Asn-26,
	1165					888																				889
	3 - 1319		•			103 - 906			-															<u>-</u>		2 - 454
	267					290					-	_														291
	928789					929193														-						931154
						HDPDA47																				HWMEV63
						280																				281

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S0358: 1 and H0580: 1.	AR061: 2, AR089: 2 S0358: 1, H0413: 1, L0502: 1, L0657: 1, H0522: 1 and H0422: 1.		AR089: 3, AR061: 1 T0042: 1, H0543: 1 and H0422: 1.
Pro-47 to Ser-61, Arg-116 to Thr-122.	Pro-19 to Lys-34, Arg-63 to Arg-72, Lys-76 to Pro-113, Gln-133 to Gln-150, Gln-152 to Gln-163, Glu-167 to Arg-187.	Lys-15 to Ser-20, Arg-51 to Arg-60, Lys-64 to Pro-101.	Leu-7 to Phe-27, Gin-50 to Gin-57.
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1-50 to	-51 to	/-78 to	-133 to	1-211 t	-239 to	r-280 t	n-347 t	0-378 1	3-390 t	r-406 t	-422 to	3-440 t	-458 to	-485 t	7-526 t												
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2260 892 Ser-39 to Pro-44, AR061: 2, AR089: Pro-51 to Thr-56, H0424: 9, L0747: 7, Gly-78 to Cys-92, H0618: 5, H0620: 5, H0549: 4, L0655: 4, His-239 to Gln-230, L079: 4, L0655: 4, His-239 to Gln-235, H0081: 3, Royad: 3, Asp-378 to Asn-385, H0083: 3, H0188: 3, Arg-390 to Gly-320, L0774: 3, L0805: 3, Royad: 3, Arg-390 to Gly-420, L0774: 3, L0805: 3, Royad: 3, Arg-440 to Leu-450, L0774: 3, L0759: 3, Royad: 2, Royad: 2, Royad: 2, H0617: 2, H0697: 2, L0772: 2, L0676: 2, L0677: 2, L0772: 2, L0803: 2, L0772: 2, L0803: 2, L0772: 2, L0384: 2, L0381: 2, L	HHFJH79 1228195 294 608 - 2260 892 Ser-39 to Pro-44, Pro-51 to Thr-56, Gly-78 to Cys-92, H0018: 5, H0024: 9, L0747: 7, Gly-78 to Cys-92, H0018: 5, H0020: 5, H0024: 9, L0747: 7, Gly-78 to Cys-92, H0018: 5, H0020: 5, H0024: 4, Glu-211 to Ala-219, H0087: 4, L0658: 4, His-239 to Gln-256, L0750: 4, S0222: 3, Thr-280 to Glu-285, H0253: 3, S0346: 3, Asn-347 to Gly-371, H0150: 3, H00181: 3, Asp-378 to Asn-385, H00283: 3, H0188: 3, Arg-390 to Gly-398, H0428: 3, H0213: 3, Thr-406 to Gly-420, L0774: 3, L0805: 3, Pro-422 to Gly-420, L0774: 3, L0769: 2, H0051: 2, H0049: 2, L0772: 2, L0372: 2, L0772: 2, L0372: 2, L0772: 2, L038: 2	HHFJH79 1228195 294 608 - 2260 892 Ser-39 to Pro-44, AR061: 2, AR089: Pro-51 to Thr-56, H0424: 9, L0747: 7, Gly-78 to Cys-92, H0618: 5, H0620: 5, H0649: 4, Glu-211 to Ala-219, H0087: 4, L0625: 4, His-239 to Glu-285, H0253: 3, S0346: 3, Asn-347 to Gly-371, H0150: 3, H0081: 3, Asn-347 to Gly-371, H0150: 3, H0188: 3, Arg-390 to Gly-398, H0428: 3, H0233: 3, H0428: 3, H0249: 4, Pro-422 to Gly-420, L0774: 3, L0805: 3, Pro-422 to Gly-420, L0774: 3, L0769: 2, H0619: 2, Pro-428 to Gly-420, L0774: 3, L0769: 2, H0619: 2, Pro-488 to Leu-490, S0049: 2, H0024: 2, H0017: 2, H0049: 2, L0778: 2,	HHFJH79 1228195 294 608 - 2260 892 Ser-39 to Pro-44, AR061: 2, AR089: Pro-51 to Thr-56, H0424: 9, L0747: 7, Gly-78 to Cys-92, H0618: 5, H0620: 5, H0549: 4, L0809: 3, H0549: 4, L0809: 3, H0619: 3, Asn-347 to Gly-371, H0150: 3, H0081: 3, Asn-347 to Gly-371, H0150: 3, H0081: 3, Asn-347 to Gly-371, H0150: 3, H0081: 3, Arg-370 to Gly-398, H0428: 3, L0808: 3, Arg-340 to Gly-40: 2, L0769: 3, L0769: 2, H0619: 2, H0649: 2, H0619: 2, H0649: 2, H0619: 2, H0649: 2, H0619: 2	HHFJH79 1228195 294 608 - 2260 892 Ser-39 to Pro-44, AR061: 2, AR089: Pro-51 to Thr-56, H0424: 9, L0747: 7, Gly-78 to Cys-92, H0618: 5, H0520: 5, H0549: 4, L0809: 3, H0549: 4, L0809: 2, H0619: 2,	HHFJH79 1228195 294 608 - 2260 892 Curl-30 to Curl-30. HHFJH79 1228195 294 608 - 2260 892 Ser-39 to Pro-44, AR061: 2, AR089: Pro-131 to Thr-24: 9, L0618: 5, H0620: 3, Gly-78 to Cys-92, H0618: 5, H0620: 3, H0620: 3, Thr-280 to Glu-285, H0553: 4, L0653: 4, His-239 to Glu-285, H0253: 3, S0346: 3, Asn-347 to Gly-285, H0253: 3, S0346: 3, Asn-347 to Gly-378, H0628: 3, H0618: 3, Arg-390 to Gly-398, H0628: 3, H0618: 3, Arg-390 to Gly-398, H0628: 3, H0619: 2, H0619: 2, H0692: 3, H06428: 4, H0619: 2, H0619: 2, H0619: 2, H06428: 4, H0619: 2, H0649: 2, L0669: 2, H0649: 2, L0669: 2	HHFJH79 1228195 294 608 - 2260 892 Gun-30 to Gun-37. HHFJH79 1228195 294 608 - 2260 892 Gun-30 to Cha-37. Gly-78 to Cys-92, H0618.5, H0620.5, H0620.5, H0618.5, H0620.5, H0620.5, H0621.2, Gly-78 to Cys-92, H0618.5, H0620.5, H0631.3, H0620.5, H0631.3, H0631.2, H0631.2, H0631.3, H0631.3, H0631.2, H06

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H0689: 1, H0690: 1, H0684: 1, H0670: 1, H0660: 1, H0648: 1, H0672: 1, S0044: 1, L0741: 1, L0743: 1, L0748: 1, L0751: 1, L0756: 1, L0752: 1, L0731: 1, L0757: 1, H0665: 1, L0096: 1 and		AR089: 4, AR061: 2 L0439: 5, S0002: 3, L0604: 3, H0619: 2, H0024: 2, H0625: 2, L0768: 2, L0757: 2, H0638: 1, S0420: 1, S0360: 1, H0586: 1, L0163: 1, S0214: 1, L0143: 1, H0264: 1, L0774: 1, L0651: 1, L0659: 1, L0542: 1, L0779: 1, L0758: 1, L0777: 1, L0758: 1,		AR089: 0, AR061: 0 H0620: 2, L0761: 2,
		Ser-30 to Ser-35.	Gln-27 to Trp-45.	Lys-6 to Trp-11, Pro-26 to Pro-40,
	1168	863	1169	894
	2 - 832	1 - 993	155 - 856	1-1119
	570	295	571	296
	933308	1155190	933357	1078092
		HUCOW17 1155190		HFKIT06
		285		286

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L0766: 2, L0744: 2, L0754: 2, L0596: 2, H0686: 1, H0295: 1, H0657: 1, H0264: 1, S0002: 1, L0769: 1, L0774: 1, L0805: 1, L0657: 1, L0790: 1, H0690: 1 and H0521:		AR089: 8, AR061: 2 S0218: 1 and H0486: 1		AR089: 2, AR061:	L0769: 3, S0354: 1, H0393: 1, H0355: 1 and	H0124: 1.		AR089: 1, AR061: 1 H0522: 2 and L0766:		AR061: 5, AR089:	L0439: 8, H0052: 7	L0741: 7, L0756: 4,	S0010: 3, H0261: 2, H0156: 2, S0049: 2,
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	1170	895	1171	968			1172	268	1173	868			:
	1 - 300	3 - 536	3 - 464	3 - 1349			2 - 427	3 - 734	3 - 734	2 - 1126			
	572	297	573	298			574	299	575	300			
	934019	1104159	934472	1082268			934505	1081629	934520	1197899			
		HDTBY88		HWLHS82				HDPNC96		HCE5I78			
		287		288				289		290			

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L0770: 2, L0776: 2, L0742: 2, L0745: 2, L0366: 2, S0222: 1, H0438: 1, H0390: 1, S0346: 1, H0009: 1, L0455: 1, S0038: 1, L0789: 1 and L0758: 1.	.		AR089: 2, AR061: 1	T0049: 1, S0278: 1,	H0031: 1 and H0339: 1.										AR089: 46, AR061: 33	H0521: 4, H0051: 2,	L0803: 2, L0748: 2,	L0740: 2, L0756: 2,	L0752: 2, L0755: 2,	_H0590: 1, H0014: 1,
Thr-150 to Thr-158, Lys-183 to Phe-193, Pro-277 to Asn-299, Asp-324 to Gly-333, Lys-354 to Glu-361, Gln-367 to Ser-374.	Pro-14 to Gln-20, Ala-29 to Ala-52,	1 yr-64 to Ser-70, Ser-103 to His-120.	Ser-39 to Trp-44,	Ile-48 to Trp-54,	Asn-65 to Asp-8/,	FIG-94 to Gill-100,	Asp-163 to His-174,	Ser-193 to His-199.	Ser-11 to Trp-16,	Ile-20 to Trp-26,	Asn-37 to Ser-58,	Leu-67 to Gln-72,	Lys-101 to Asp-108,	Asp-135 to Tyr-140.	Met-7 to Ser-12,	Ser-20 to Arg-30,	Asp-85 to Ala-92,	Met-119 to Asn-146,	Pro-151 to Asp-161,	Gln-253 to Glu-260,
	1174		668						1175						006					
	3 - 422		182 - 862						1-519						210 - 1697					
	576		301						577						302					
	934531		1159625				-	,	935932	,,					1212566					
			HISDS62						•						69ЛОООН					
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S0250: 1, L0772: 1, L0764: 1, L0804: 1, H0522: 1, S0406: 1, L0754: 1, L0779: 1, L0731: 1 and L0758: 1.			AR061: 8, AR089: 4	20471: 1, L0772: 1,	.0529: 1 and L0780: 1.	AR089: 12, AR061: 4	H0598: 1 and H0135:					AR089: 3, AR061: 2	H0597: 1, H0435: 1	and H0543: 1.						AR061: 2, AR089: 1	H0013: 3, L0439: 2,	[0624: 1, H0171: 1,	S0040: 1, S0420: 1,
Ile-333 to Val-342, Solution So		Lys-1 to Thr-7, Arg-34 to Pro-41.	Q.	<u>, </u>		₹		Leu-204 to Thr-220.	Lys-49 to Lys-54,	Trp-106 to Lys-112,	Leu-130 to Gly-141.	Ser-3 to Thr-11, A		Thr-50 to Glu-57, an	Thr-83 to Gln-88.	Ser-3 to Thr-11,	Lys-32 to Gly-39,	Thr-50 to Glu-57,	Thr-83 to Gln-88.			Asp-70 to Phe-84, H	Val-94 to Ser-101, S
	1176	1177	901			905			1178			903				1179				904			
	2 - 829	551 - 339	1 - 351			2 - 661			3 - 440			284 - 703	-			88 - 474				2 - 577			
	578	579	303			304			280			305				581				306			
	937850	949702	939957			1088554			942673			1184003			•	944057				1031741			
	I		HEMBT61			HRODZ70						HHERQ79								HCECM90			
			293			294						295								296			

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H0619: 1, H0156: 1, H0575: 1, H0590: 1, H0052: 1, H0011: 1, H0266: 1, H0494: 1, L0519: 1, H0519: 1, H0555: 1, L0777: 1, L0758: 1, S0436: 1 and H0506: 1.							AR054: 23, AR050:	16, AR051: 3, AR089:	1, AR061: 1	H0586: 1 and L0375:	1.									
Ala-112 to Ser-125, Lys-140 to Asn-145, Asn-175 to Tyr-180, Arg-187 to Thr-192.	Gly-12 to Gly-31, Asn-38 to Gly-62,	Asp-70 to Phe-84, Val-94 to Ser-101,	Ala-112 to Ser-125,	Lys-140 to Asn-145,	Asn-175 to Tyr-180,	Arg-187 to Thr-192.	Lys-63 to Pro-72,	Val-97 to Gly-102,	His-116 to Cys-123,	Tyr-161 to Thr-167,	Pro-204 to Lys-210,	Ala-214 to Lys-222,	Glu-276 to Lys-289,	Tyr-305 to Thr-312,	Pro-383 to Gly-398.		Gly-1 to Gly-7,	Ala-13 to Gln-21,	Ala-43 to Ser-48,	Asn-67 to Gly-75,
	1180						908									1181	1182			
	2 - 577						3 - 1208									100 - 939	327 - 1			
	582						307							-		583	584			
	945088						1199614									945692	947361			
							HWHGW72													
							297				_									

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	AR089: 0, AR061: 0		AR050: 8, AR054: 6,		AR061: 1	H0036: 2, L0766: 2,	H0686: 1, H0622: 1,	H0625: 1, L0791: 1,	L0779: 1 and S0434: 1.													AR050: 21, AR054: 9,	AR051: 3, AR089: 1,	AR061: 1	H0553: 4 and L0759:	7.	
Pro-82 to Pro-90.	Thr-1 to Leu-12, Asp-107 to Thr-114,	Thr-1 to Leu-12.	Glu-9 to Ser-20,	Ile-23 to Gly-29,	Pro-50 to Cys-66,	Pro-74 to Glu-79,	Glu-93 to Trp-98,	Thr-121 to Ser-133,	Leu-180 to Lys-196,	Thr-213 to Glu-225,	Glu-234 to Glu-240,	Arg-263 to Glu-270,	Glu-283 to Ala-298,	Lys-318 to Ala-336,	Val-340 to Ala-351,	Val-361 to Pro-372,	Asn-445 to Pro-468,	Pro-475 to Lys-491.	Thr-1 to Ala-10,	Val-20 to Pro-31,	Asn-104 to Thr-124.	Gln-97 to Pro-114,	Trp-117 to Lys-129,	Thr-166 to Gln-173,	Ser-178 to Lys-183,	Glu-250 to Phe-256,	Ser-295 to His-301,
	906	1183	907																1184			806					
	123 - 875	112 - 417	85 - 1557					-											3 - 452			1287 - 292		4			
	308	585	309																586			310					
	1219890	945856	946988												•				972348			947484					
	HPCRV84		HNSAA28																			HLWAR77					
	298		299																			300					

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	AR061 3 AR089 2	3, L0803: 3,	L0748: 3, L0749: 3,	H0574: 2, H0046: 2,	L0794: 2, L0776: 2,	L0439: 2, L0754: 2,	L0747: 2, L0755: 2,	L0605: 2, L0593: 2,	H0686: 1, S0360: 1,	L0717: 1, H0069: 1,	H0575: 1, H0620: 1,	H0024: 1, S0388: 1,	H0510: 1, H0266: 1,	H0644: 1, H0163: 1,	H0090: 1, H0634: 1,	H0561: 1, H0695: 1,	L0763: 1, L0804: 1,	L0774: 1, L0775: 1,	L0659: 1, L0783: 1,	L0809: 1, L0666: 1,	L0665: 1, L0438: 1,	H0519: 1, H0658: 1,	H0539: 1, S0152: 1,	H0522: 1, L0740: 1,	L0777: 1, L0603: 1,	S0276: 1 and H0542: 1.	
Tyr-307 to Gln-316,	Glu-522 to Ser-530. Phe-8 to Gln-13	Arg-63 to Gly-69,	Gly-135 to Lys-144,	Ala-201 to Ala-211,	Arg-248 to Thr-255,	Leu-294 to Pro-299.																					Val-11 to Gly-21, Gly-72 to Thr-80.
	606	\ \ \																									1185
	423 - 1319											-															25 - 660
	311	1			•			_																			587
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	HTTIW49																										
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AR089: 4, AR061: 3 H0581: 3, H0622: 3, H0575: 2, H0090: 2, L0777: 2, L0757: 2, S0114: 1, H0650: 1, H0255: 1, S0360: 1, S0278: 1, H0486: 1, H0318: 1, H0457: 1, H0039: 1, H0553: 1, L0763: 1, L0761: 1, L0764: 1, L0789: 1, H0144: 1, S0374: 1, S0310: 1, H0555: 1, L0758: 1, H0445: 1 and S0276: 1.		AR089: 14, AR061: 9 H0457: 1, H0009: 1, L0666: 1, S0053: 1 and L0741: 1.		AR089: 4, AR061: 2 L0744: 9, L0747: 8, S3014: 7, L0740: 7, S0192: 6, S0027: 5, S0212: 4, H0124: 4,
Pro-1 to Pro-7, Leu-10 to Lys-18, Val-119 to Lys-126, Gln-146 to Trp-151.	Pro-1 to Pro-7, Leu-10 to Lys-18, Val-119 to Lys-126, Gln-146 to Trp-151, Asp-210 to Arg-216.			Thr-28 to Lys-34, Pro-36 to Asn-44, Lys-72 to Lys-83.
910	1186	911	1187	912
54 - 1718	54 - 791	1 - 669	192 - 494	1 - 249
312	588	313	589	314
1155193	948434	1082762	948533	1180374
HWAFS18		HFCBA44		HVADT77
302		303		304

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L0731: 4, L0662: 3, L0743: 3, L0752: 3,	L0759: 3, H0662: 2,	H0575: 2, H0545: 2,	H0041: 2, H0413: 2,	L0775: 2, H0696: 2,	L0748: 2, L0751: 2,	L0754: 2, L0749: 2,	L0758: 2, H0445: 2,	S0276: 2, H0624: 1,	L0778: 1, L0005: 1,	H0645: 1, H0441: 1,	H0391: 1, S0005: 1,	T0040: 1, H0069: 1,	H0427: 1, S0280: 1,	H0042: 1, T0048: 1,	H0505: 1, H0309: 1,	H0544: 1, H0009: 1,	H0266: 1, H0617: 1,	H0412: 1, H0623: 1,	T0004: 1, L0564: 1,	T0041: 1, H0494: 1,	H0633: 1, H0646: 1,	H0652: 1, L0769: 1,	L0646: 1, L0655: 1,	L0659: 1, L0546: 1,	L0783: 1, L0809: 1,	H0144: 1, L0565: 1,	S0126: 1, H0689: 1,	H0435 1 H0659: 1.
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H0672: 1, S0378: 1, H0555: 1, S0037: 1, S0206: 1, L0777: 1, L0780: 1, S0434: 1, S0011: 1, S0194: 1 and H0506: 1.						AR089: 2, AR061: 2	H0441: 5, H0134: 3,	H0050: 2, S0038: 2,	L0777: 2, H0583: 1,	H0650: 1, H0656: 1,	H0255: 1, H0125: 1,	H0192: 1, H0676: 1,	H0438: 1, S0049: 1,	H0038: 1, H0529: 1,	H0690: 1, L0439: 1,	1100//: 1 and fig300: 1.							AR061: 4, AR089: 4	L0439: 4, L0418: 1,
	Thr-11 to Trp-25,	Ser-35 to Arg-42,	Asp-50 to Arg-56,	Tyr-75 to Ser-81,	Gly-89 to Gln-104.	Cys-7 to Ala-24,	Asn-30 to Asn-42,	Ser-80 to Ser-89,	•	Leu-142 to Ser-150,		Arg-234 to Trp-240.					Cys-7 to Ala-24,	Asn-30 to Asn-42,	Ser-80 to Ser-89,	Leu-130 to Arg-135,	Leu-142 to Ser-150,	Tyr-161 to Arg-166.	Gly-14 to Glu-32,	Pro-60 to Ala-70,
	1188					913						_					1189						914	
	1 - 330					25 - 858											25 - 924						3 - 509	
	590					315										,	591						316	
	948886					1189013										1000	949137						951351	
		*				HUFCN91																	HAGBX32	
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172471, 186580, 264800, 266600, 278760, 600760, 600761, 600761, 600761,		·	
S0028: 1 and L0741: 1.		AR061: 1, AR089: 1 L0748: 2, H0171: 1, S0134: 1, S0354: 1, S0358: 1, H0014: 1, H0083: 1, H0510: 1, L0764: 1, L0803: 1, L0789: 1, H0593: 1, H0659: 1, H0593: 1, H0555: 1, L0751: 1, L0758: 1, L0759: 1 and L0595: 1.	AR061: 3, AR089: 2 L0439: 21, L0438: 12, L0769: 9, T0010: 6,
Thr-145 to Gly-153, Ser-164 to Leu-169.	Phe-4 to Gly-12.	Ile-94 to Asp-99, Asp-118 to Pro-123, Glu-131 to Ile-140, Tyr-143 to Asp-152, Glu-169 to Lys-179. Ile-94 to Asp-99, Asp-118 to Pro-123, Glu-131 to Ile-140, Tyr-143 to Asp-152, Glu-169 to Lys-179.	Ser-3 to Lys-8, His-29 to Lys-38, Pro-201 to Thr-206.
	1190	915	916
	473 - 138	3 - 572	1 - 795
	592	593	318
	956281	955336	1156430
		HWMIB81	HCEMU86
		307	308

H0052: 5, L0776: 4, L0805: 3, S0126: 3, L0741: 3, L0589: 3, H0261: 2, T0006: 2, L0455: 2, L0659: 2, H0519: 2, L0742: 2, L0748: 2, L0751: 2, L0592: 2, S0276: 2, H0583: 1, L0418: 1, S0229: 1, S0001: 1, S0229: 1, H0156: 1, H0331: 1, H0156: 1, L0351: 1, S0352: 1, L0598: 1, L0369: 1, L0520: 1, L0777: 1, L0752: 1, L0753: 1, L0758: 1, L0593: 1 and		AR051: 23, AR050: 20, AR054: 11, AR061: 9, AR089: 5 S0250: 8, S0126: 8, H0251: 3, H0545: 2,
	His-26 to Lys-35, Pro-198 to Thr-203.	
	5 1192	917
	2520 - 1735	368 - 3
	594	319
	956864	1153911
		HRDAF83
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H0252: 2, L0794: 2, L0565: 2, L0744: 2, L0757: 2, S0040: 1, S0212: 1, S0418: 1, S0360: 1, H0549: 1, H0024: 1, L0053: 1, H0124: 1, S0208: 1,	2			58: 4,	2: 3,	1: کې	5: 2,	4: 2,	8: 2,	9: 2,	3: 2,	6: 1,	8: 1,	6: 1,	1:1,	2: 1,	6: 1,	23: 1,	0: 1,	2: 1,
H0252: 2, L0794: 2, L0565: 2, L0744: 2, L0757: 2, S0040: 1, S0212: 1, S0418: 1, S0360: 1, H0549: 1, H0024: 1, L0053: 1, H0124: 1, S0208: 1,			2, AR061:	L0789: 4, L0758: 4,	H0657: 3, H0052: 3,	L074	T000	H019	H0046: 2, H0038: 2,	.0800: 2, L0659: 2,	H0521: 2, L0743: 2,	H055	S0282: 1, S0358: 1	, H058	H0618: 1, H0231: 1,	S0362: 1, H0622: 1	H061	, H062	L0351: 1, S0150: 1	L0769: 1, L0372:
52: 2, 65: 2, 57: 2, 112: 1, 24: 1, 24: 1, 11: 11:			AR089:	789: 4	57: 3,	38: 3,	79: 3,	81: 2,	46: 2,	00:2,	521: 2,	39: 2,	82: 1,	519: 1,	518: 1	62: 1,	06: 1,	113: 1	51: 1,	69: 1,
H02 L03 L07 S03 S03 H00 H01 S03	<u> </u>	Ι	AR	<u> </u>	90H	<u>1</u>	L07	H05	H0(F08	H05	101	S02	HOH	HO	S03	T00	70H	<u> </u>	101 101
	71,	50, 73.	Ő,	92,	-179,	-200,	-217,	-243.												
	o Val-	Arg-	His-2	o Asp-	to Phe	to Ser	to Ala	to Ser												
	Asn-66 to Val-71. Glu-82 to Thr-91.	Ser-42 to Arg-50, Gln-66 to Val-73	Pro-14 to His-20,	Gln-82 to Asp-92,	Ser-161 to Phe-179,	Cys-190 to Ser-200,	Gln-212 to Ala-217,	Glu-235 to Ser-243.												
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	344	-3	1288			_														
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L0662: 1, L0794: 1, L0775: 1, L0651: 1, L0527: 1, L0657: 1, L0666: 1, H0547: 1, H0690: 1, H0658: 1, H0672: 1, H0539: 1, S0378: 1, H0555: 1, L0754: 1, L0747: 1, L0780: 1, L0596: 1, S0192: 1, H0542: 1 and H0423: 1.		AR089: 13, AR061: 5	H0617: 6, H0556: 4,	H0305: 3, S0007: 3,	H0618: 3, H0521: 3,	L0439: 3, H0672: 2,	L0754: 2, L0600: 2,	S0442: 1, S0354: 1,	S0358: 1, S0045: 1,	S0046: 1, S0222: 1,	H0438: 1, H0587: 1,	H0599: 1, H0036: 1,	H0597: 1, H0530: 1,	L0118: 1, H0570: 1,	H0023: 1, S0250: 1,	H0039: 1, H0181: 1,	H0674: 1, S0036: 1,	L0351: 1, T0041: 1, H0494: 1, H0509: 1.
	Asn-89 to Asn-95.	Asp-1 to Gly-12,	Ala-24 to Gln-29,	Ala-43 to Asn-61,	Ala-68 to Gly-81,	Pro-84 to Gln-99,	Glu-105 to Gln-110,	Ala-118 to Asp-123,	Arg-170 to Leu-175,	Pro-296 to Thr-306,	Asn-311 to Gln-320,	Arg-327 to Ala-335,	Asp-382 to Gly-389,	Ala-441 to Pro-451,	Val-464 to Cys-491,	Ser-495 to Gly-504,	Asp-509 to Trp-516,	Gly-518 to Pro-527.
	1195	919																
	83 - 439	3 - 1646																
	597	321																
	959020	1197921																
		HSCKS55																
		311																

L0769: 1, L0761: 1, L0764: 1, L0768: 1, L0806: 1, H0519: 1, H0593: 1, H0670: 1, H0660: 1, S3014: 1, L0741: 1, L0779: 1 and H0667: 1.					AR061: 9, AR089: 5	S0356: 17, S0212: 6,	L0747: 6, S0360: 5,	H0486: 5, S0418: 3,	H0551: 3, S0040: 2,	S0354: 2, H0599: 2,	H0544: 2, H0617: 2,	H0413: 2, S0210: 2,	L0794: 2, S0126: 2,	S0037: 2, S0027: 2,	L0743: 2, H0665: 2,	S0192: 2, S0196: 2,	S0116: 1, H0662: 1,	S0420: 1, H0619: 1,	H0550: 1, H0013: 1,	H0618: 1, H0253: 1,	H0251: 1, H0546: 1,	H0545: 1, H0086: 1,	H0123: 1, H0024: 1,
	Pro-72 to Thr-82,	Asn-87 to Gln-96,	Arg-103 to Ala-111,	Asp-158 to Gly-165.	Ala-8 to Gly-14,	Gly-32 to Arg-48,	Ala-58 to Asn-66,	Glu-82 to Gln-92,	Arg-101 to Gly-110,	Thr-124 to Asp-131,	Trp-137 to Gly-146,	Leu-153 to His-160,	Glu-171 to Lys-177,	Asp-191 to Ser-196,	Glu-225 to Gly-233,	Glu-248 to Glu-253,	Thr-259 to Trp-265,	Arg-268 to Asp-277,	Glu-303 to Arg-311,	Ala-329 to Leu-343.			
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	703 - 1704				2 - 1030																		
	865				322																		
	961074				963290	-																	
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H0286: 1, H0252: 1, H0628: 1, S0294: 1, L0372: 1, L0646: 1, L0773: 1, L0806: 1, L0654: 1, L0790: 1, L0565: 1, H0689: 1, H0670: 1, H0660: 1, S0028: 1, S0032: 1, L0749: 1, L0777: 1, L0749: 1, L0777: 1, L0780: 1, L0595: 1, H0668: 1, H0667: 1, S0276: 1, S0424: 1 and H0352: 1.	AR089: 4, AR061: 1 L0751: 4, H0052: 3, S0024: 3, S0364: 3, L0438: 3, L0439: 3, H0657: 2, L0415: 2, H0438: 2, H0156: 2, H0373: 2, L0455: 2, H0529: 2, L0664: 2, H0144: 2, L0749: 2, L0592: 2, H0422: 2, L0692: 1, H0583: 1, H0656: 1, S0045: 1, S0046: 1, L0717: 1, H0261: 1, H0455: 1, H0261: 1, H0575: 1,
	Phe-2 to Asp-13, Ser-47 to Gly-52, Arg-161 to Asp-167, Leu-256 to Leu-261, Asp-288 to Asn-296.
	921
·	2704 - 1739
	323
	1193149
	HBODE51
	313

S0346: 1, H0581: 1, H0251: 1, H0046: 1, H0009: 1, H0050: 1, S0003: 1, S0214: 1, S0366: 1, H0316: 1, H0598: 1, L0351: 1, S0150: 1, L0643: 1, L0764: 1, L0662: 1, L0794: 1, L0662: 1, L0653: 1, L0659: 1, L0653: 1, H0521: 1, S0146: 1, H0345: 1, H0478: 1, H0345: 1, L0745: 1, L0758: 1, L0745: 1, L0667: 1, S0194: 1, H0542: 1, S0194: 1, H0542: 1,	
S0346: 1 H0251: H0009: H0014: S0003: S0366: H0598: S0150: L0764: L0764: L0764: L0666: H0539: S0146: H0478: L0745: L0588: S0026: S0194: H0677:	
	Gln-12 to His-20, Val-34 to Tyr-39, Asn-54 to Asn-59, Asp-105 to Gly-110, Gly-247 to Lys-256, Gln-314 to Gly-320, Arg-359 to Ser-366, Arg-420 to Gly-428, Ala-558 to Tyr-563, Leu-574 to Pro-579,
	Gln-12 to His-20, Val-34 to Tyr-39, Asn-54 to Asn-59 Asp-105 to Gly-1 Gly-247 to Lys-2, Gln-314 to Gly-3; Arg-359 to Ser-3(Arg-420 to Gly-4, Ala-558 to Tyr-56 Leu-574 to Pro-5
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		AR089: 3, AR061: 2	L0666: 8, L0439: 6,	H0253: 5, H0046: 4,	L0769: 4, H0295: 3,	H0255: 3, L0747: 3,	L0756: 3, L0779: 3,	H0657: 2, H0618: 2,	H0318: 2, H0622: 2,	H0068: 2, L0667: 2,	L0772: 2, L0776: 2,	L0663: 2, H0520: 2,	H0593: 2, H0670: 2,	H0521: 2, L0750: 2,	L0759: 2, L0593: 2,	L0601: 2, S0116: 1,	H0341: 1, S0212: 1,	H0306: 1, H0402: 1,	L0617: 1, S0358: 1,	H0609: 1, H0592: 1,	H0333: 1, T0040: 1,	H0013: 1, H0635: 1,	H0575: 1, H0036: 1,	H0581: 1, H0123: 1,	H0071: 1, T0010: 1,	H0687: 1, H0290: 1,	H0617: 1, H0606: 1,
Arg-592 to Phe-597,	Ala-621 to Arg-630, Pro-636 to His-641.	Tyr-47 to Glu-58,	Lys-70 to Gly-77,	Pro-121 to Leu-126,	Leu-150 to Leu-158,	Asn-166 to Glu-171,	Arg-417 to Ser-425,	Phe-465 to Cys-473,	Ser-485 to Asn-492,	Ser-497 to Ala-504,	Gln-531 to Trp-537,	Asp-557 to Glu-562.	•														
		922																									
		2692 - 389																									
		324																									
		965304											_														
L		HHFCK09				1000																					
		314	_																								

																				
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H0038: 1, H0487: 1, H0494: 1, H0334: 1, S0150: 1, H0647: 1, S0142: 1, L0640: 1, L0639: 1, L0637: 1,	20641: 1, L0768: 1, 20649: 1, L0514: 1, 20659: 1, L0783: 1,	L0788: 1, L0664: 1, L0665: 1, L0438: 1,	H0547: 1, H0455: 1, H0522: 1, H0696: 1,	S0404: 1, H0478: 1,	.0742: 1, L0740: 1,	749: 1, L0758: 1,	S0454: 1, S0194: 1, H0422: 1 and H0506: 1.	AR089: 15, AR061: 5	H0662: 2, H0670: 1,	LU/56: 1 and LU/59: 1.	- 1	AR089: 1, AR061: 0	H0521: 15, H0638: 5,	H0580: 5, H0271: 5,	H0641: 5, H0560: 4,	H0090: 3, H0591: 3,	766: 3, H0542: 3,	H0543: 3, H0586: 2,)497: 2, H0581: 2,	L0655: 2, H0518: 2,
S01 S01 L06				S02				AR	H	3	-	AR	<u> </u>	E E	, HO	E	្ឋ			
								Asp-43 to Glu-48.	4		Asp-43 to Glu-48.	Lys-7 to Gly-69,	Lys-82 to Lys-88,	Ser-94 to Asp-112,	Ala-126 to Asp-131	Tyr-134 to Ser-140,	Ser-147 to Phe-156,	Asp-159 to Ser-165,	Thr-176 to Asp-186,	Glu-230 to Leu-250,
						•		923			1198	924								
								89 - 943			89 - 592	72 - 1202	,					•		
								325			009	326								
								1110364)))		965306	1119032								
								HCOOZ11 1110364				HDPPO35								
								315	3			316								

H0522: 2, L0754: 2, L0747: 2, H0657: 1, H0393: 1, H0431: 1, H0250: 1, H0635: 1, L0021: 1, H0014: 1, H0179: 1, H0416: 1, H0488: 1, L0475: 1, H0359: 1, H0625: 1, S0426: 1, L0598: 1, L0667: 1, L0803: 1, L0667: 1, L0659: 1, L0792: 1, L0663: 1, S0428: 1, H0672: 1, H0555: 1, H0445: 1 and S0424: 1.	
Glu-291 to Arg-298, Gln-313 to Glu-320, Asn-331 to Gly-343, Ser-348 to Leu-363.	Lys-7 to Gly-69, Lys-82 to Lys-88, Ser-94 to Asp-112, Ala-126 to Asp-131, Tyr-134 to Ser-140, Ser-147 to Phe-156, Asp-159 to Ser-165, Thr-176 to Asp-186, Glu-230 to Leu-250, Glu-291 to Arg-298, Glu-291 to Glu-313, Asn-331 to Glu-320, Asn-331 to Gly-343, Ser-348 to Leu-363.
	1199
	72 - 1202
	601
	966248

AR089: 5, AR061: 2 L0439: 13, L0752: 4, L0015: 3, H0144: 2, L0438: 2, L0742: 2, L0747: 2, L0758: 2, H0556: 1, L0785: 1, S0001: 1, H0664: 1, H0580: 1, H0486: 1, T0060: 1, H0253: 1, S0010: 1, H0564: 1, L0471: 1, S0051: 1, H0412: 1, L0370: 1, L0763: 1, L0768: 1, L0763: 1, L0768: 1, L0776: 1, L0806: 1, L0776: 1, H0520: 1, R0659: 1, H0187: 1, H0659: 1, H0187: 1,		AR089: 18, AR061: 5 L0740: 11, L0439: 9, L0748: 8, H0616: 5, L0666: 5, L0601: 5, S0444: 4, L0776: 4, L0659: 4, L0744: 4, L0747: 4, L0749: 4,
		Gly-11 to Thr-16, Ser-35 to Ser-56, Thr-58 to Ser-73, Tyr-85 to Asp-91, Glu-100 to Glu-109.
925	1200	926
2 - 1126	2 - 1126	100 - 501
327	602	328
157542	968602	1197910
HLWDZ53 1157542		HEOPL36
317		318

L0755: 4, H0457: 3, L0774: 3, L0750: 3,	H0624: 2, T0002: 2,	S0116: 2, S0358: 2,	H0550: 2, T0040: 2,	H0013: 2, H0599: 2,	H0050: 2, H0673: 2,	H0038: 2, H0040: 2,	H0494: 2, L0770: 2,	L0662: 2, L0364: 2,	L0375: 2, L0809: 2,	L0438: 2, H0547: 2,	L0754: 2, L0756: 2,	L0752: 2, L0731: 2,	L0758: 2, L0485: 2,	S0040: 1, H0583: 1,	H0650: 1, H0657: 1,	H0341: 1, H0663: 1,	H0580: 1, H0619: 1,	L0717: 1, H0574: 1,	H0052: 1, H0263: 1,	H0009: 1, H0172: 1,	H0024: 1, T0010: 1,	H0510: 1, H0644: 1,	S0036: 1, H0551: 1,	H0264: 1, H0488: 1,	H0056: 1, H0100: 1,	L0564: 1, T0041: 1,	H0652: 1, S0344: 1,	S0002: 1, L0763: 1,	T 0638.1 T 0761.1
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L0372: 1, L0643: 1, L0764: 1, L0768: 1, L0381: 1, L0775: 1, L0526: 1, L0782: 1, L0663: 1, L0665: 1, H0703: 1, H0520: 1, H0435: 1, H0521: 1, S0044: 1, L0751: 1, L0757: 1, L0751: 1, L0757: 1, L0759: 1, H0445: 1, L0584: 1,				AR061: 2, AR089: 0	L0766: 10, L0794: 7,	L0758: 7, L0805: 6,	L0751: 4, L0754: 4,	L0803: 3, L0483: 2,	L0764: 2, L0659: 2,	L0809: 2, L0790: 2,	L0666: 2, L0755: 2,	L0599: 2, H0170: 1,	H0294: 1, H0583: 1,	H0656: 1, S0282: 1,	H0255: 1, S0420: 1,	H0618: 1, H0688: 1,	L0055: 1, S0344: 1,
	Gly-11 to Thr-16, Ser-35 to Ser-56	Thr-58 to Ser-73,	Tyr-85 to Asp-91,	Leu-42 to Gln-49,	Gln-59 to Thr-65,	Pro-119 to Lys-128,	Asn-134 to Phe-140,	Arg-150 to Phe-155,	Asp-205 to Gly-212.								
	1201		-	927													
	85 - 486			3 - 734													
	603			329													
	968826			1152252											•		
		•		HMCFS02													
				319													_

H0529: 1, L0761: 1, L0643: 1, L0645: 1, L0804: 1, L0806: 1, L0653: 1, L0776: 1, L0629: 1, L0636: 1, L0788: 1, L0789: 1, L0791: 1, L0665: 1, S0428: 1, H0702: 1, L0438: 1, S0330: 1, H0539: 1, H0478: 1, L0779: 1, L0750: 1, L0779: 1, L0731: 1, L0779: 1, L0731: 1, L0757: 1, H0665: 1 and H0423: 1.		AR061: 2, AR089: 2 L0759: 12, L0439: 11, L0766: 7, L0775: 5, H0521: 5, L0755: 5, L0748: 4, L0756: 4, L0777: 4, L0731: 4, L0581: 4, L0619: 3, L0666: 3, L0779: 3, L0757: 3, L0588: 3, S0418: 2, L0618: 2, H0580: 2, L0773: 2, L0769: 2, L0773: 2,
	Arg-3 to Lys-20, Phe-22 to Ser-28,	Leu-50 to Gln-57. Pro-26 to Leu-34, His-42 to Asn-51, Phe-154 to Pro-162, His-237 to Asp-246, Pro-263 to Lys-268, Lys-277 to Asp-282, Pro-285 to Leu-295, Pro-305 to Asp-312.
	1202	928
	2 - 496	178 - 1167
	604	330
	969326	1194752
		HDPSR15
		320

L0747: 2, L0750: 2, H0265: 1, H0663: 1, S0356: 1, H0208: 1, H0370: 1, H0108: 1, H0575: 1, H0618: 1, H0544: 1, H0545: 1, H0286: 1, H0631: 1, H0494: 1, L0564: 1, H0494: 1, L0475: 1, L0763: 1, L0761: 1, L0763: 1, L0768: 1, L0662: 1, L0768: 1, L0662: 1, L0768: 1, L0663: 1, H0519: 1, L0663: 1, H0519: 1, H0435: 1, L0751: 1, L0749: 1, L0751: 1, L0749: 1, L0603: 1,		AR054: 10, AR089: 2, AR061: 1, AR051: 1, AR050: 1 H0305: 1, H0580: 1, H0428: 1, L0803: 1,
	Pro-26 to Leu-34, His-42 to Asn-51.	Pro-1 to Lys-6.
	1203	929
	168 - 785	1104 - 697
	909	331
	999696	1217231
		HNTAV78
		321

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L0809: 1 and H0519: 1.			AR061: 3, AR089: 2	L0792: 2, H0012: 1,	H0100: 1, L0663: 1,	L0756: 1 and L0780: 1.		AR051: 3, AR050: 1,	AR089: 1, AR061: 0	H0521: 3, H0656: 2,	H0635: 2, H0549: 1,	H0050: 1, H0413: 1,	H0641: 1, L0387: 1,	H0436: 1 and H0423: 1.	AR054: 34, AR051:	29, AR050: 23, AR089:	4, AR061: 4] HU013: 1		
	Glu-52 to Leu-58,	Arg-63 to Lys-71, Arg-83 to Val-88.	Ala-2 to Pro-9,	Val-22 to Gly-28.			Ala-5 to Gly-18.	Asp-1 to Asn-10.							His-8 to Gly-18,	Glu-150 to Leu-167.			His-8 to Gly-18,	Glu-150 to Leu-167.
	1204		930				1205	931							932				1206	
	3 - 266		3 - 1319				15 - 1733	182 - 1312							14 - 544				14 - 544	
	909		332				209	333							334				809	
	971315		1145842			_	974255	974711							1094875				974911	
			HFKDR14 1145842					HDPBI30							HODFF88					
			322					323							324	-				

- [37] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.
- [38] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.
- [39] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.
- [40] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A.

It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

- [41] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.
- [42] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is

assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[43] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIMTM (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID	SEQ ID	CONTIG	BAC ID: A	SEQ ID	EXON
NO:Z	NO:X	ID:		NO:B	From-To
HCEPH71	14	522739	AL365319	1207	1-494
HCEPH71	14	522739	AL390715	1208	1-494
HLMDO95	43	928344	AC020641	1209	1-591
					627-2046
HTEAG49	54	954614	AL390796	1210	1-1310
HTEAG49	54	954614	AL357045	1211	1-1310
HTEAG49	54	954614	AL390796	1212	1-627
HTEAG49	54	954614	AL357045	1213	1-627
HACCH94	103	847143	AL161458	1214	1-1140
HACCH94	103	847143	AL161458	1215	1-90
		1	1		5811-6312
HFKLX38	113	880220	AL136383	1216	1-32
]	1288-1454
					1561-1646
	Ì				3840-4700
		1	1		5482-6798
HTDAB17	117	890384	AC011078	1217	1-297
		j		}	359-416
					3247-3653
			Ì	ĺ	6083-6236
	ł		1		9753-10036
i				i.	11128-11233
					12148-12514
					12635-13141
			1		15604-16463
				Ì	19071-19190
		}		}	19476-20232
					20321-20638
					21200-21594
					21959-22219
	1				23120-23362
	1				23467-24143
				}	24766-24853
					25725-26143
					26310-26455
					27545-30619
					30708-31169
HTLCA95	142	911655	AC012616	1218	1-1151
HTLCA95	142	911655	AC012616	1219	1-284
ННЕНС53	152	921783	AC009427	1220	1-100
					1854-1942
				1	3236-3463
]			4629-4868

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					5054-5181
					5371-5476
				1	5851-5953
Ì				1	6104-6149
				1	6509-6612
ļ	ļ				7131-8415
					8429-8492
	-				8638-8748
	İ				8975-9440
1				1	9835-10490
]		.)			10606-10899
					11149-11282
					11382-11881
				İ	12023-12075
					12172-12315
		ļ			12496-12551
					12638-12706
ĺ					12827-12994
					13077-13630
HHEHC53	152	921783	AC009427	1221	1-428
HHEHC53	152	921783	AC009427	1222	1-388
					466-526
					698-906
Í					1023-1922
HELHF07	196	949067	AC073669	1223	1-597
HELHF07	196	949067	AC023605	1224	1-583
HELHF07	196	949067	AC074220	1225	1-362
HELHF07	196	949067	AC074220	1226	1-105
HACAD35	199	949199	AC007363	1227	1-98
ļ					3271-3413
}		1			4132-4357
		Į			7030-7682
]		<u> </u>	j	}	11881-12001
					12874-13485
HDTKQ14	254	886936	AL359542	1228	1-140
					1249-4264
HDTKQ14	254	886936	AL359542	1229	1-499
HDTKQ14	254	886936	AL359542	1230	1-145
HWAGS73	257	894404	AL096870	1231	1-185
{				[393-1743
	1	1			1951-2118
					2229-2295
		}	j	}	2410-2906
					3043-3107
-					3238-3519
					3594-3970
HWAGS73	257	894404	AL096870	1232	1-1080
j					2072-2811

HCVDV22	270	909846	AC004084	1233	1-105
HSYBX32	270	909840	AC004064	1233	839-1021
					2069-2302
ł	}	}			2470-2855
					3818-4265
				.	4371-4610
	}				4761-4810
	}				5364-5802
					5930-6517
	}				7073-7807
		,			8063-8618
	1				8636-8875
			,		9438-9537
					10568-10774
					10897-11025
Ì					11718-12323
					13749-13849
					13978-14188
	1				14474-14554
	j				16489-16624
					16924-17019
					17239-17458
]				17908-18185
				ı	19014-19266
					19356-19451
	ļ		j		19620-19873
					19893-20920
					21092-21247
					21512-21579
					21621-21754
					22001-22831
					22992-23518
					23710-24370
					24426-24596
					25213-25493
	ļ				25661-26192
					26588-27433
					27598-27742
			_		28073-28199
					28359-28651
	1	,			28777-29249
					29379-29502
					29646-29794
	1				29833-30033
					30085-30630
					30702-32661
				!	33104-33374
				,	33383-33661
L		L	L	L	23333 33331

HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004951 1237 1-25		·				
HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004084 1237 1-25						33808-33871
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25						33978-37449
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25				1		37587-37754
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25				1		38296-38433
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25						38597-39343
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25)	40047-40395
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25						40462-40743
HSYBX32 270 909846 AC004084 1235 1-28 HSYBX32 270 909846 AC004951 1237 1-25						40938-41039
HSYBX32 270 909846 AC004951 1234 1-73 HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004084 1237 1-25	i I	}	1			41187-41634
HSYBX32 270 909846 AC004951 1234 1-73 991-154 HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004951 1237 1-25 1-25 1-25 1	 				1	42504-42687
HSYBX32 270 909846 AC004951 1234 1-73 HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004951 1237 1-25	1			}]	42703-42850
991-154 HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004951 1237 1-25	L					42929-43475
HSYBX32 270 909846 AC004084 1235 1-23 HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004951 1237 1-25	HSYBX32	270	909846	AC004951	1234	1-735
HSYBX32 270 909846 AC004084 1236 1-28 HSYBX32 270 909846 AC004951 1237 1-25	L					991-1547
HSYBX32 270 909846 AC004951 1237 1-25	HSYBX32	270	909846	AC004084	1235	1-239
	HSYBX32	270	909846	AC004084	1236	1-283
HSYBX32 270 909846 AC004951 1238 1-31	HSYBX32	270	909846	AC004951	1237	1-255
	HSYBX32	270	909846	AC004951	1238	1-318
HTLJC71 284 922923 AC009516 1239 1-200	HTLJC71	284	922923	AC009516	1239	1-2009
HTLJC71 284 922923 AC007957 1240 1-174	HTLJC71	284	922923	AC007957	1240	1-1747
HTLJC71 284 922923 AC018751 1241 1-200	HTLJC71	284	922923	AC018751	1241	1-2009
HTLJC71 284 922923 AC023490 1242 1-200	HTLJC71	284	922923	AC023490	1242	1-2009
HTLJC71 284 922923 AC009516 1243 1-37	HTLJC71	284	922923	AC009516	1243	1-375
HTLJC71 284 922923 AC009516 1244 1-49	HTLJC71	284	922923	AC009516	1244	1-494
HTLJC71 284 922923 AC007957 1245 1-20	HTLJC71	284	922923	AC007957	1245	1-205
HTLJC71 284 922923 AC018751 1246 1-49	HTLJC71	284	922923	AC018751	1246	1-494
HTLJC71 284 922923 AC023490 1247 1-37	HTLJC71	284	922923	AC023490	1247	1-375
HTLJC71 284 922923 AC018751 1248 1-37	HTLJC71	284	922923	AC018751	1248	1-375
HWMEV63 291 931154 AC078816 1249 1-157	HWMEV63	291	931154	AC078816	1249	1-1574

[45] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

FABLE 2

Clone ID	Contig	SEQ	Analysis	PFam/NR Description	PFam/NR Accession	Score/	NT	NT
Z:ON	Ë	E	Method	-	Number	Percent	From	To
HTPAD46	503313	335	HMMER	PFAM: Src homology	PF00018	4.14	160	186
HCWFF88	206577	336	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.92	140	181
HSSAX53	507509	337	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.36	266	331
НСЕРН71	522739	14	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.22	33	62
HTEDF74	522982	338	HMMER 1.8	PFAM: C2 domain	PF00168	86.9	189	233
HTTEK47	573649	339	HMMER 1.8	PFAM: EF hand	PF00036	10.82	224	289
			blastx.2	DJ534K7.2 (novel protein).	sp CAB92087 CAB9 2087	100% 65% 52%	283	301 378 410
HTOBE75	591896	340	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	61.2	100	273
HCFAT05	592118	341	HMMER 2.1.1	PFAM: Ion transport protein	PF00520	106.1	137	361
			blastx.2	potassium channel protein [Homo sapiens]	gb AAA59457.1	67% 100% 52%	134	427
HFIAH37	615597	342	HMMER	PFAM: C2 domain	PF00168	4.22	241	291

			1.8					
HFTDF15	657020	343	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.85	168	203
HPFCU80	685294	344	HMMER 1.8	PFAM: C2 domain	PF00168	4	261	296
HSVAW49	689674	345	HMMER 1.8	PFAM: Src homology domain 3	PF00018	36.33	11	169
			blastx.2	(AF146277) adapter protein CMS [Homo sapiens]	gb AAD34595.1 AF1 46277_1	97%	65	166
НЖНОС94	1116463	23	blastx.14	(AC004472) P1.11659_3 [Homo sapiens]	gi 2984587 gb AAC0 7985.1	76%	581 476	874 547
НЖНОС94	715096	346	HMMER 1.8	PFAM: C2 domain.	PF00168 ·	4.17	214	300
			blastx.2	Pig-o.	sp BAA96254 BAA9 6254	64%		627
HRSMD49	723025	347	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.76	199	270
HFTDY67	1151220	25	blastx.14	(AF182316) myoferlin [Homo sapiens]	gi 6731235 gb AAF27 176.1 AF182316 1	94%	1368	52
				•		33%	201	94
,						42%	63 201	145
HFTDY67	745221	348	HMMER 1.8	PFAM: C2 domain	PF00168	20.07	4	144
			blastx.2	Myoferlin.	sp AAF27177 AAF27	%86	4	225
	·				177	100%	224	298
HYABL89	786157	349	HMMER	PFAM: C2 domain	PF00168	6.05	270	317

			1.8					
HCUEV29	1137791	27	blastx.14	(AL110490) predicted	gi 5824799 emb CAB	23%	96	344
				using Genefinder	54442.1	53%	387	470
				[Caenorhabditis elegans]		64%	9	47
HCUEV29	816065	350	HMMER 1.8	PFAM: EF hand	PF00036	31.87	143	229
			blastx.2	CG10641 PROTEIN.	sp Q9VJ26 Q9VJ26	59% 49%	89 312	286
HCESP56	827671	351	HMMER 1.8	PFAM: EF hand	PF00036	11.86	240	317
			blastx.2	HYPOTHETICAL 27.4 KDA PROTEIN (FRAGMENT).	sp Q9UJF6 Q9UJF6	100%	186	452
HLQDT35	839777	352	HMMER 1.8	PFAM: Src homology domain 3	PF00018	3.85	342	419
			blastx.2	(AK000579) unnamed protein product [Homo saniens]	dbj BAA91269.1	%86	252	458
HDPBS64	846624	30	HMMER 1.8	PFAM: Thioredoxins	PF00085	116.87	173	493
			blastx.2	ZK973.11 protein.	sp AAF40013 AAF40 013	32%	182	652
HTBAB41	867287	353	HMMER 1.8	PFAM: C2 domain	PF00168	5.32	68	157
HTLGE31	870247	32	HMMER 1.8	PFAM: Sugar (and other) transporters	PF00083	21.4	5	115
НWLНК29	1152279	33	blastx.14	(AF181098) synaptotagmin IV	gi 5823558 gb AAD5 3186.1 AF181098_1	27% 29% 30%	474 198 77	602 371 166
				Lytosophina metanogastri		9/00		201

73lghlA	PF00168 gil3452473lgblAAC7		domain	HMMER PFAM: C2 domain 1.8 blastx.14 (AF084205)	4 HMMER PFAM: C2 domain 1.8 (AF084205)
ا			(AF 084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	blastx.14 (AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	54 blastx.14 (AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]
	rotein PF00069	PFAM: Eukaryotic protein PF00069 kinase domain		IMER PFAM: Eukaryotic protein kinase domain	HMMER PFAM: Eukaryotic protein 1.8 kinase domain
I [л.Р- sp 043374 043374	٥'		PUTATIVE RASGAP-	blastx.14 PUTATIVE RASGAP-
		ACTIVATING-LIKE PROTEIN.	ACTIVATING-LIKE PROTEIN.	ACTIVATING-LIKE PROTEIN	PROTEIN.
∞	PF00168	PFAM: C2 domain PF0016		PFAM: C2 domain	HMMER PFAM: C2 domain 1.8
82		PFAM: Src homology PF000 domain 3		PFAM: Src homology domain 3	HMMER PFAM: Src homology 1.8 domain 3
\D2 -1	2 gb AAD27647.1 AF1 ns] 36380 1	(AF136380) SH3P12 gb AA protein [Homo sapiens] 36380	ls]	(AF136380) SH3P12 protein [Homo sapiens]	(AF136380) SH3P12 protein [Homo sapiens]
sp 097902 097902				DIFFERENTIATION	blastx.14 DIFFERENTIATION
	TOR	ENHANCING FACTOR	ENHANCING FACTOR	ENHANCING FACTOR	ENHANCING FACTOR
)18	y PF00018	rc homology	IMER PFAM: Src homology	PFAM: Src homology	HMMER PFAM: Src homology
			domain 3	domain 3	domain 3
790	N sp 097902 097902		-	DIFFERENTIATION	DIFFERENTIATION
	TOR	ENHANCING FACTOR	ENHANCING FACTOR	ENHANCING FACTOR	ENHANCING FACTOR

HOHCE47	911566	359	HMMER	PFAM: Eukaryotic protein	PF00069	79.42	211	423
			1.8	kinase domain			· !)
69IIQSH	917180	360	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.09	382	429
HKAKM10	1227639	40	blastx.14	NUCLEAR BODY ASSOCIATED KINASE	8 8 8 8 8	%88	6	284
HKAKM10	918685	361	HMMER	2B. PFAM: Eukaryotic protein	PF00069	31.4	∞	127
HCEPU56	920347	362	2.1.1 HMMFR	kinase domain PFAM: C2 domain	DE00168	,	5	Coc
) }	1.8	i i i i i i i i i c c dollidili	0,100,11	5.75	743	567
			blastx.2	HYPOTHETICAL 27.3 KDA PROTEIN.	sp O60362 O60362	82%	219	659
HUSHB54	928054	42	HMMER 1.8	PFAM: C2 domain	PF00168	20.52	275	355
	928344	43	HMMER	PFAM: 7 transmembrane	PF00001	43.25	220	369
HLMD095			1.8	receptor (rhodopsin family)				
			blastx,2	Inflammation-related G	sp AAF91467 AAF91	51%	112	375
				protein-coupled receptor EX33.	467	%56	375	446
HHASQ32	928730	363	HMMER	PFAM: Carnitate	PF00755	317	250	855
			2.1.1	acyltransferase				
HARAB87	1164340	45	blastx.14	neurotransmitter	gi 914028 gb AAB32	%68	51	350
				transporter rB21a [rats,	806.1	83%	349	549
				brain, Peptide, 616 aa]		%06	16	45
			ţ	[Rattus sp.]			-	
HARAB87	933441	364	HMMER	PFAM:	PF00209	9.67	268	570
			2.1.1	Sodium:neurotransmitter				

				symporter family				
HTNGF69	933614	365	HMMER 1.8	PFAM: C2 domain	PF00168	3.94	588	659
HMSJL96	1154788	47	blastx.14	(AF104413) large tumor suppressor 1 [Homo sapiens]	gi 4324434 gb AAD1 6882.1	80% 86% 41%	1 1282 1085	124 5 137
								1117
HMSJL96	934483	366	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	26.49	199	363
HDTBT06	935404	367	HMMER 2.1.1	PFAM: Actin	PF00022	110.8	514	903
			blastx.2	actin-related protein - fruit fly (Drosophila melanogaster)	pir S44028 S44028	47%	52	876
HTTIE47	1165363	49	blastx.14	ZK550.2 [Caenorhabditis elegans]	gi 3881745 emb CAB 05312.1	43% 30% 34%	188 398 559	382 544 627
HTTIE47	941834	368	HMMER 1.8	PFAM: Sugar (and other) transporters	PF00083	32.12	295	522
			blastx.2	predicted using Genefinder; Similarity to worm multidrug resistance proteins [Caenorhabditis elegans]	emb CAB01157.1	38%	151	537
HHFBP47	946668	20	HMMER 1.8	PFAM: Sugar (and other) transporters	PF00083	25.74	969	370
			blastx.2	(AL050350) dJ261K5.1 (novel organic cation	emb CAB56524.1	%86 %86	482 135	955 461

				transporter (BAC ORF		100%	38	139
				RG331P03)) [Homo		77%	451	516
				sapiens]				
HCCCC81	1083553	51	blastx.14	(AL022605) putative	gi 3080435 emb CAA	%05	125	304
				protein [Arabidopsis	18752.1	%89	428	514
				thaliana		%95	302	397
				,		29%	588	689
						38%	514	591
					-	20%	334	369
	949062	369	HMMER	PFAM:	PF00202	178.37	187	816
HCCCC81			1.8	Aminotransferases class-				
				III pyriuovai-piiospiiaic				
			blastx.2	hypothetical protein	pir T25848 T25848	46%	190	879
				T01B11.2 -				
			:	Caenorhabditis elegans				
HPJEV71	949153	370	HMMER	PFAM: von Willebrand	PF00092	47.98	998	137
			1.8	factor type A domain				5
			blastx.2	CDNA FLJ10601 FIS,	sp BAA91707 BAA9	23%	974	153
117711	1136101	53	bloom 14	coltmotin Ciondio	4707 cil13002411abl A B B	708C	061	112
nieiro/	1130171	CC	DidStA.14	caluacum [Olaiula	girst-1777741 goldeno	7000	107	711
				ıntestinalis	3294.1	0/07	040	792
HTEIL07	953803	371	HMMER	PFAM: EF hand	PF00036	11.27	192	263
			- 1	TT	00 V 01970100 V 0100	7002	7.2	202
			blastx.2	Hypothetical 41.3 KDa protein.	sp CAB91065 CAB9 1065	19%	75	392
HTEAG49	954614	54	HMMER	PFAM: Src homology	PF00018	4.51	312	238
			1.8	domain 3	1			
HSLCF96	637670	55	HMMER	PFAM: Sugar (and other)	PF00083	10.78	415	929
			1.8	transporters				

			blastx.2	(AE000352) putative transport profein	gb AAC75728.1	94%	415	117
				[Escherichia coli]		200	1101	413
				, .		20%	409	121
			-			76%	1021	
								009
								117
HSLCF96	954777	372	HMMER 18	PFAM: Sugar (and other)	PF00083	30.03	1296	101
			Floaty 2	(AE000352) mitotive	25 A A C75778 11	7070	202	, [
			Ulasta.2	(ALOUDOS) purante	goldan goldan	90.06	1147	711
				[Escherichia coli]			-	121 5
HNHCI32	861673	95.	HMMER	PFAM: 7 transmembrane	PF00001	133.17	195	545
			1.8	receptor (rhodopsin				
				family)				
			blastx.2	G protein-coupled	sp AAF27279 AAF27	100%	189	551
				receptor 57.	279	100%	112	186
		·				100%	99	112
HNHCI32	956105	373	HMMER	PFAM: 7 transmembrane	PF00001	133.17	951	601
,			1.8	receptor (rhodopsin family)			-	
			blastx.2	(AF112461) G protein-	gb AAF27279.1 AF1	100%	555	917
				coupled receptor 57	12461_1	100%	478	552
				[Homo sapiens]		100%	422	478
HPMFL08	695656	374	HMMER	PFAM: Src homology	PF00018	4.97	209	238
			1.8	domain 3.		ŕ		
HTXRA13	959622	58	HMMER 2.1.1	PFAM: C2 domain	PF00168	51.3	540	608

			blastx.2	GRANUPHILIN-A.	sp Q9R0Q1 Q9R0Q1	42%	429	109
HCE3H71	1197898	59	blastx.14	SEIZURE-RELATED	sp Q62223 Q62223	%68	413	961
				PROTEIN 6 TYPE 2		%56	12	413
				PRECURSOR.		27%	126	266
						34%	150	263
,						%95	363	410
					-	39%	365	448
						41%	216	266
	·					. 43%	273	320
						36%	383	448
						46%	410	448
						. 57%	410	451
HCE3H71	189196	375	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	79.2	317	496
			blastx.2	seizure-related protein	pir 152657 152657	%88	5	685
				SEZ-6 precursor - mouse		64%	292	957
						30%	86	496
						48%	929	100
		_						0
HUTSF11	620996	376	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	27.74	3	104
HTEGI48	1021235	19	blastx.14	(AF074606) histone	gi 4091980 gb AAC9	87%	_	525
				acetyltransferase [Homo sapiens]	9368.1			
HTEGI48	530595	377	HMMER 2.1.1	PFAM: Zinc finger, C2HC type	PF01530	43.8	344	436
HSFAM09	573345	378	HMMER 1.8	PFAM: Src homology domain 3	PF00018	5.33	195	218
HNFHK77	1182286	63	blastx.14	succinic semialdehyde	gi 147901 gb AAC36	100%	180	647

	dehydrogenase);e	831.1	%16	653	868
	Escherichia coli	coli				
379 HMMER P 2.1.1	PFAM: Aldehyde dehydrogenase family	nyde e family	PF00171	30.2	231	326
x.14	No definition line found [Escherichia coli]	line found	gi 912476 gb AAB18 565.1	%58	93	969
380 HMMER 2 1 1	PFAM: Aldehyde	ıyde e family	PF00171	46.2	58	207
blastx.14	(AE000506) putative	outative	gi 2367379 gb AAC7	100%	-	106
	transport protein, cryptic,	ein, cryptic,	7312.1			∞
	orf, joins former yjiZ and	ner yjiZ and				
	yjjL [Escherichia coli]	chia coli]				
IMER	PFAM: Sugar (and other)	r (and other)	PF00083	19.71	5	538
1.8	transporters					
blastx.2	(AE000506) putative	putative	gb AAC77312.1	100%	∞	107
	transport protein, cryptic,	ein, cryptic,	,	;		5
	orf, joins former yjiZ and	ner yjiZ and	-	·		
	yjjl [Escherichia coli]	chia coli				
382 HMMER I	PFAM: Sugar (and other) transporters	r (and other)	PF00083	11.23	1595	108
blastx.2	(AE000506) putative	putative	gb AAC77312.1	100%	3	104
	transport protein, cryptic,	ein, cryptic,				6
	orf, joins former yjiZ and yjjL [Escherichia coli]	ner yjiZ and chia coli]				
MER	PFAM: Carnitate	tate	PF00755	168.4	2	445
7.1.1	acyltransierase	e.				
blastx.14	contains similarity to C2	larity to C2	gi 1825586 gb AAB4	39%	∞	241
	domains [Caenorhabditis	norhabditis	2222.1	30%	548	646
	elegans]		-	43%	551	298
	, ,		•	%96	617	589

D9764675 D11701

HMGR774	678707	384	HMMER 1 8	PFAM: C2 domain	PF00168	35.46	8	181
1777CIAIII			blastx.2	CG15078 PROTEIN.	sp Q9V8M4 Q9V8M 4	20%	8	289
698ННМН	690442	385	HMMER 1.8	PFAM: Src homology domain 3	PF00018	31.65	91	255
	. ,		blastx.2	(AF178432) SH3 protein [Homo saniens]	gb AAF35985.1 AF1 78432-1	70%	91	315
HFXLC69	692773	386	HMMER 1.8	PFAM: C2 domain	PF00168	17.77	84	200
HBXBW40	1156765	70	blastx.14	Protein Kinase [Rattus	gi 2077934 dbj BAA1	93%	214	546
				norvegicus]	9880.1	78%	546	587
HBXBW40	706115	387	HMMER	PFAM: Eukaryotic protein	PF00069	34.01	280	423
110011	1140400	ï	1.8	Kinase domain	07 4 4 4 11 (103800).	7010	(,,,
HCEILSI	1140498	./1	blastx.14	carnitine	g1/294521 gb AAA40	51%	3	233
				palmitoyltransferase I	876.1	26%	288	434
			,	[Rattus norvegicus]				
HCE1L51	715899	388	HMMER	PFAM: Carnitate	PF00755	102.9	33	434
			2.1.1	acyltransferase				
	717358	389	HMMER	PFAM: Eukaryotic protein	PF00069	23.7	14	124
HRADM45		•	1.8	kinase domain				
			blastx.2	(AJ271722) putative	emb CAB71146.1	%86	2	469
				serine/threonine protein				
				kinase MAK-V [Homo			•	
			·	sapiens]				
HTEF045	1153918	73	blastx.14	Munc13-3 [Rattus	gi 1763306 gb AAB3	94%	64	597
				norvegicus]	9720.1			
HTEF045	723446	390	HMMER	PFAM: C2 domain	PF00168	30.64	111	383
			1.0			 :		

HOHBN82	1152271	74	blastx.14	(AF182316) myoferlin	gi 6731235 gb AAF27	94%	92	140
				[Homo sapiens]	176.1 AF182316_1	87%	1418	∞
						33%	1259	146
						47%	1397	2
						79%	1259	136
				,				9
							-	145
		•						6
					-			131
								5
HOHBN82	724322	391	HMMER 1.8	PFAM: C2 domain	PF00168	49.95	96	347
,			blastx.2	Myoferlin.	sp AAF27176 AAF27	%08	93	623
					176	28%	571	909
HWHGF52	1217026	22	blastx.14	GUANINE	sp Q64096 DBS_MO	73%	14	271
-				NUCLEOTIDE	USE	19%	338	439
				EXCHANGE FACTOR		27%	∞	73
				DBS (DBLS BIG				
				SISTER) (MCF2				
				TRANSFORMING				
				SEQUENCE-LIKE				
				PROTEIN).				
	726102	392	HMMER	PFAM: Src homology	PF00018	5.01	325	387
HWHGF52			1.8	domain 3				
•		٠	blastx.2	Dbs=Dbl guanine	gb AAB33461.1	74%	3	203
				nucleotide exchange		72%	319	417
			•	factor homolog [mice,		73%	203	259
				32D 1				
HBKDI30	1223861	92	blastx.14	BA243J16.3 (similar to	sp CAC10006 CAC1	100%	343	672
				MYLK (myosin, light	9000	91%	23	307

				polypeptide 1			-	
HBKDI30	729048	393	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	42.23	1	213
HSQFR54	1185143	LL	blastx.14	vacuolar protein sorting	gi 1477468 gb AAC5	%98	52	882
				homolog r-vps33a [Rattus	2985.1	94%	1134	164
				norvegicus		%96	798	>
						92%	1640	113
				,		31%	1332	7
								183
								7
								146
HSQFR54	730964	394	HMMER 2.1.1	PFAM: Sec1 family	PF00995	66.1	2	259
			blastx.2	VACUOLAR PROTEIN SORTING HOMOLOG	sp Q63615 Q63615	%98	2	310
				R-VPS33A.				
HAGBA56	1102593	78	blastx.14	(AF033655) Pftaire-1	gi 2645810 gb AAB8	%56	187	735
				[Mus musculus]	7504.1	28%	_	153
		·				79%	132	203
HAGBA56	732597	395	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	64.9	139	516
HHSAE29	1220851	62	blastx.14	probable sugar transport	pir S47743 S47743	100%	572	946
	-	,		protein - Escherichia coli		%56	1021	108
HHSAE29	743166	396	HMMER	PFAM: Sugar (and other)	PF00083	44.67	29	250
			1.8	transporters				
	746582	80	HMMER	PFAM: Src homology	PF00018	11.08	316	405
HMSH064			1.8	domain 3				
			blastx.2	(AF030131) Plenty of	gb AAC40070.1	47%	-	411

. ,				SH3s; POSH [Mus musculus]				,
HFPBW22	750631	397	HMMER 1.8	PFAM: C2 domain	PF00168	61	323	430
HTLBH67	751985	398	HMMER 1.8	PFAM: Src homology domain 3	PF00018	37.78	16	162
HNTMH70	1143523	83	blastx.14	similar to protein kinases	gi 1072163 gb AAA8	20%	425	299
				[Caenorhabditis elegans]	11690.1	40%	101	220
						29%	344	445
			- 1			41%	70	174
HNTMH70	757184	399	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	94.55	176	577
нсетс59	761881	400	HMMER 2.1.1	PFAM: Sec1 family	PF00995	60.4	117	305
<u> </u>			blastx.2	Vacuolar protein sorting	sp AAF91174 AAF91	%8 <i>L</i>	123	368
				33B.	174	100%	<i>L</i> 9	123
						64%	311	412
HE8UX76	1161223	85	blastx.14	(AB026803)	gi 6136784 dbj BAA8	%86	437	108
				synaptotagmin VI [Mus	5775.1	91%	86	7
				musculus]		%16	1129	454
						36%	692	138
						34%	1129	c
								841
								124
НЕ8UX76	767871	401	HMMER 1.8	PFAM: C2 domain	PF00168	7.23	592	636
HTLEN77	1136124	98	blastx.14	(AF081671) VU91D calmodulin [synthetic	gij3800851 gb AAC6 8892.1	43%	240	392
				construct]				

D9764875 D11701

HTLEN77	772363	405	HMMER	PFAM: EF hand	PF00036	26.93	294	380
			1.8					
			blastx.2	CALTRACTIN (CENTRIN).	sp P53441 CATR_N AEGR	30%	1111	374
HBGDI80	1124695	87	blastx.14	(AL078627) actin-like protein; (2 actin domains)	gi 5051483 emb CAB 44762.1	46%	5	328
				[Schizosaccharomyces pombe]	*:			
HBGDI80	781600	403	HMMER 2.1.1	PFAM: Actin	PF00022	33.6	52	318
			blastx.2	CG7940 PROTEIN.	sp Q9VEC3 Q9VEC3	37%	13	336
HELHB88	811935	404	HMMER 1.8	PFAM: EF hand	PF00036	12.8	247	330
			blastx.2	INTERSECTIN LONG	sp Q9UNK2 Q9UNK	84%	139	567
-				ISOFORM.	2	46%	145	375
					-	100%	78	146
\dashv						30%	361	495
HTEMV66	1152261	68	blastx.14	contains EGF-like repeats;	gi 495684 gb AAA50	%95	265	621
				highly similar to ZC84.1;	735.1	44%	61	195
HTEMV66	813038	405	HMMER	PFAM: Eukaryotic protein	PF00069	27.8	154	315
			2.1.1	kinase domain				
HMTAJ73	813296	406	HMMER	PFAM: Eukaryotic protein	PF00069	21.34	4	114
十			1.8	kinase domain				
HE9TD31	815845	91	HMMER 1.8	PFAM: EF hand	PF00036	17.53	519	909
-			blastx.2	Intersectin 2 short	sp AAF59904 AAF59	81%	3	626
				isoform.	904	40%	378	979
HGBDG55	1141363	92	blastx.14	(AF004161) peroxisomal	gi 2352427 gb AAB6	62%	209	529

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				[Mus musculus]	9748.11	47%	472	522
06ДІОДН	831976	411	HMMER 1.8	PFAM: EF hand	PF00036	10.08	413	496
			blastx.2	Intersectin 2.	sp AAF63600 AAF63	87%	206	694
					000	0/00	717	3
HFRBN81	1182552	26	blastx.14	(AE000192) putative	gi 1787127 gb AAC7	%66	2163	298
				transport [Escherichia	3985.1			
				colı				
HFRBN81	833061	412	HMMER	PFAM: Sugar (and other)	PF00083	35.69	52	420
			1.8	transporters				
			blastx.2	Hypothetical protein Y	dbj BAA35630.1	100%		1111
				[Escherichia coli]				9
HFRBN81	973206	413	HMMER	PFAM: Sugar (and other)	PF00083	30.84	52	393
,			1.8	transporters				
· .			blastx.2	Hypothetical protein Y	dbj BAA35630.1	%08	4	546
				[Escherichia coli]	,		,	
HFRBN81	973208	414	blastx.2	Hypothetical protein Y	dbj BAA35630.1	%26	2	352
				[Escherichia coli]		75%	351	587
						18%	56	229
HFKJW01	1187134	86	blastx.14	lactaldehyde	gi 145222 gb AAA23	100%	394	∞
				dehydrogenase	427.1			
				[Escherichia coli]				
HFKJW01	836491	415	HMMER	PFAM: Aldehyde	PF00171	174	96	440
		-	2.1.1	dehydrogenase family				
		*****	blastx.2	lactaldehyde	pir A38165 A38165	100%	96	440
				dehydrogenase (EC				•
		• .	-	1.2.1.22) aldA -				
				Escherichia coli				
HSDFL63	836498	416	HMMER	PFAM: Aldehyde	PF00171	127.4		234

			2.1.1	dehydrogenase family				-
			blastx.2	RETINALDEHYDE- SPECIFIC	sp O94788 DHAS_H UMAN	%001	·	249
				DEHYDROGENASE				
				TYPE 2 (EC 1.2.1)				
				(RALDH(II)) (RALDH-				
				2).				
HPJET90	836503	100	HMMER	PFAM: Aldehyde	PF00171	150.4	99	371
			2.1.1	dehydrogenase family				
	836514	101	HMMER	PFAM: Aldehyde	PF00171	397.1	10	642
HEMFC61			2.1.1	dehydrogenase family				
			blastx.2	RETINALDEHYDE-	H_SAHD[887490]qs	%86	4	642
				SPECIFIC	UMAN			
				DEHYDROGENASE	-			
				TYPE 2 (EC 1.2.1)				
				(RALDH(II)) (RALDH-	•	•		
				2).				
HDTBR50	1174351	102	blastx.14	intermediate chain 1 [Anthocidaris crassispina]	gi 1817526 dbj BAA0 9934.1	57%	130	306
	846630	417	HMMER	DFAM: Thioredovins	PE00085	29.95	163	707
HDTBR50	00000) . F	1.8	11 AIVI: 1 IIIIOICAUAIIIS	110000	67.65	501	1/7
	-		blastx.2	NM23-H8.	sp AAF20909 AAF20	100%	130	327
					606	97%	327	467
	847143	103	HMMER	PFAM: 7 transmembrane	PF00001	167.94	10	735
HACCH94			1.8	receptor (rhodopsin family)			-	
			blastx.2	ORPHAN G PROTEIN- COUPLED RECEPTOR.	sp 095853 095853	%66	7	879
HE8TI39	849161	418	HMMER	PFAM: EF hand	PF00036	12.66	6	98
			1.8					

			blastx.2	CDNA FLJ11040 FIS,	sp BAA91969 BAA9	%86	3	371
				CLONE PLACE1004388.	6961	64%	299	685
						63%	627	719
HEGAP32	851207	419	HMMER 1.8	PFAM: C2 domain	PF00168	33.03	=	172
			blastx.2	SYNAPTOTAGMIN	sp Q9R0N6 Q9R0N6	85%	50	238
				VIII.		%06	270	299
				,		%02	241	270
HCWFU66	853005	106	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	71.4	105	569
HUSYI29	853149	107	HMMER 2.1.1	PFAM: Sec1 family	PF00995	108.8	. 3	332
			blastx.2	VACUOLAR PROTEIN	sp Q63615 Q63615	%56	3	314
				SORTING HOMOLOG	,	93%	403	591
				R-VPS33A.		%06	335	394
	_					31%	. 87	221
HMEFT66	1134131	108	blastx.14	(AF121859) sorting nexin	gi 4689258 gb AAD2	46%	754	606
				9 [Homo sapiens]	7832.1 AF121859_1	40%	193	324
	-					21%	142	183
						41%	688	738
HMEFT66	856149	420	HMMER 1.8	PFAM: Src homology domain 3	PF00018	28.51	Ω.	136
HKAAR71	863023	109	HMMER 1.8	PFAM: C2 domain	PF00168	16.26	309	551
			blastx.2	TOLLIP PROTEIN.	691060 691060 ds	78%	147	959
H7TBC95	865922	011	HMMER	PFAM: 7 transmembrane	PF00001	189.5	3	695
			2.1.1	receptor (rhodopsin family)				
-			blastx.2	G-protein coupled	sp BAA93001 BAA9	999	516	701

				receptor SALPR.	3001	%19	51	206
		-		-		41%	303	440
H7TBC95	908115	421	HMMER	PFAM: 7 transmembrane	PF00001	189.5	3	695
			2.1.1	receptor (rhodopsin family)				
			blastx.2	angiotensin II receptor	gb AAC59635.1	34%	9	695
				[Xenopus laevis]				
HAPPX52	872075	422	HMMER	PFAM: Sugar (and other)	PF00083	37.84	72	359
			1.8	transporters				
HBGSJ13	1152326	1112	blastx.14	ferrienterobactin receptor	gi 1778500 gb AAB4	94%	-	753
,				precursor [Escherichia	0783.1		·	
				coli]				
HBGSJ13	878322	424	HMMER	PFAM: Src homology	PF00018	4.07	445	510
			1.8	domain 3				
			blastx.2	ferrienterobactin receptor	gb AAB40783.1	95%	64	684
r			-	precursor [Escherichia				-
				coli				
HFKLX38	880220	113	HMMER	PFAM: PMP-	PF00822	103.9	6	299
			2.1.1	22/EMP/MP20/Claudin				
	•			family				
			blastx.2	(AF087825) claudin-7	gb AAD09760.1	44%	3	299
				[Mus musculus]				-
HTLGP15	1165362	114	blastx.14	(AF060173) SV2 related	gi 3901268 gb AAC7	%88	301	786
				protein [Rattus	8627.1			
				norvegicus]				
HTLGP15	880297	425	HMMER	PFAM: Sugar (and other)	PF00083	34.17	291	590
			1.8	transporters		,		
HMEGH46	887791	426	HMMER 1.8	PFAM: C2 domain	PF00168	12.81	10	78
•	_	-	-					-

			blastx.2	GLUT4 VESICLE	sp Q9Z1X5 Q9Z1X5	%09	7	216
				PROTEIN	,	20%	40	216
				(FRAGMENT).				
HE8PY29	1129488	1116	blastx.14	(AF100751) FK506-	gi 5410288 gb AAD4	100%	. 2	277
				binding protein FKB23 isoform [Homo sapiens]	3015.1			, <u></u> .
HE8PY29	887862	427	HMMER	PFAM: EF hand	PF00036	13.65	191	250
			1.8					
			blastx.2	FK506-BINDING PROTEIN.	sp Q9Y6B0 Q9Y6B0	100%	2	277
	890384	1117	HMMER	PFAM: Thioredoxin	PF00085	107.9	276	533
HTDAB17			2.1.1				-	
·			blastx.2	CG1837 PROTEIN.	VYV99999999999999999999999999999999999	42%	225	518
			-		3	43%	231	539
						41%	348	533
HCFCF47	894415	428	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	89.54	20	295
НДОНВ19	895106	429	HMMER	PFAM: Eukaryotic protein	PF00069	92.5	260	520
			2.1.1	kınase domain				_
HAGDN53	1129154	120	blastx.2	PALS1.	sp AAF63789 AAF63 789	%16	3	293
	895963	430	HMMER	PFAM: Src homology	PF00018	22.95	270	335
HAGDN53			1.8	domain 3				
	-		blastx.2	coded for by C. elegans	gb AAA96115.1	43%	165	455
				cDNA yk34a9.5; coded		38%	103	156
				for by C. elegans 1			_	
				elegans]				
HUFDB74	1162672	121	blastx.14	phosphoinositide-specific	gi 1195552 gb AAA8	28%	170	547
				phospholipase C [catfish,	7954.1	%69	2	160

HUFDB74 901451 431 HNHFH24 1092567 122 HNHFH24 903741 432 HBGQT03 908173 433 HETLF29 1103959 124 HETLF29 1103959 434	HMMER 2.1.1 blastx.2 HMMER 2.1.1	PFAM: Phosphatidylinositol- specific phospholipase C,			,	-
1092567 122 903741 432 908173 433 1103959 124	2.1.1 blastx.2 HMMER 2.1.1	Phosphatidylinositol-specific phospholipase C, Y domain	PF00387	89.4	7	127
1092567 122 903741 432 908173 433 1103959 124	blastx.2 HMMER 2.1.1	specific phospholipase C, Y domain				
1092567 122 903741 432 908173 433 1103959 124 1 909762 434	blastx.2 HMMER 2.1.1	Y domain				
903741 432 908173 433 908173 433 1103959 124	blastx.2 HMMER 2.1.1					
903741 432 908173 433 1103959 124 134	HMMER 2.1.1	PRO1722.	sp AAF69605 AAF69	28%	806	156
903741 432 908173 433 1103959 124	HMMER 2.1.1		605	%89	763	632
908173 433	2.1.1	PFAM:	PF00209	37.2	208	306
908173 433		Sodium:neurotransmitter				
908173 433		symporter family				
908173 433	blastx.14	(AF075266) orphan	gi 3347930 gb AAC2	%9L	187	327
908173 433		transporter isoform B9	7761.1	27%	414	467
908173 433 1103959 124 909762 434		[Mus musculus]				
1103959 124	HMMER	PFAM: SH3 domain	PF00018	68.5	.615	785
1103959	2.1.1					
1103959	blastx.2	(AF130979) SH3 domain-	gb AAF04472.1 AF1	93%	ω,	791
1103959		containing protein 6511	30979_1			
1103959 9 909762		[Homo sapiens]				
909762	blastx.14	(AJ250839)	gi/7160989 emb CAB	%26	3	482
909762		serine/threonine protein	76471.1			
909762		kinase [Homo 1				
	HMMER	PFAM: Eukaryotic protein	PF00069	143.18	9	416
	1.8	kinase domain		,		
	blastx.14	similar to cAMP-	gi 3878636 emb CAA	%95	9	416
		dependant protein kinase;	88953:1			
		cDNA EST 1 1 1				
909797 435	HMMER	PFAM:	PF00387	118.2	202	453
HOUGD29	2.1.1	Phosphatidylinositol-		,	,	
		specific phospholipase C,				

				Y domain				
			blastx.14	(AF044576)	gi 2957270 gb AAC3	42%	202	753
				phospholipase C PLC210	8963.1	35%	757	873
-				[Caenorhabditis elegans]		28%	168	203
HTEMV09	1128254	126	blastx.14	protein kinase I [Rattus norvegicus]	gi 406113 gb AAA19 670 11	44%	-	321
HTEMV09	909843	436	HMMER	PFAM: Eukaryotic protein	PF00069	99.16	19	312
			blastx.14	protein kinase I [Rattus	gi 406113 gb AAA19	44%	-	321
				norvegicus	670.1			
HNTNB14	1128964	127	blastx.14	calmodulin-binding	gi 349075 gb AAA16	%86	42	476
				protein [Rattus	633.1	47%	979	929
				norvegicus		33%	587	929
HNTNB14	909942	437	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	96.28	38	343
,			blastx.14	calmodulin-binding	gi 349075 gb AAA16	%16	41	475
				protein [Rattus	633.1	85%	553	657
				norvegicus]		74%	553	657
,						77%	553	657
						%69	559	657.
						%59	553	657
						%09	553	657
					-	52%	553	654
						37%	553	657
	•					39%	553	989
						35%	553	645
						33%	559	657
,						17%	512	538
						29%	556	657
HE2KZ07	1149808	128	blastx.14	(AB004267)	gi 3135197 dbj BAA2	92%	17	508

	-			Ca2+/calmodulin-	8263.1			
				dependent protein kinase I	-			
				beta 2 [Rattus norvegicus]	,			
HE2KZ07	909948	438	HMMER	PFAM: Eukaryotic protein	PF00069	115.19	5	289
			1.8	kinase domain				
			blastx.14	(AB004267)	gi 3135197 dbj BAA2	%96	17	433
				Ca2+/calmodulin-	8263.1	%95	418	507
				dependent protein kinase I				
				beta 2 [Rattus norvegicus]				
HSIGN57	1105444	129	blastx.14	(AB033615)	gi 6705987 dbj BAA8	%96	3	962
				phospholipase C-L2 [Mus	9457.1	%02	982	104
				musculus]				_
HSIGN57	910078	439	HMMER	PFAM:	PF00387	159.3	131	484
			2.1.1	Phosphatidylinositol-				
				specific phospholipase C,				•
				Y domain				
			blastx.2	PHOSPHOLIPASE C-L2.	sp Q9QYG1 Q9QYG	83%	2	754
HLHBC30	1106654	130	blastx.14	1-phosphatidylinositol-	pir S14113 S14113	85%	6	332
				4,5-bisphosphate		77%	408	512
				phosphodiesterase 1		85%	155	175
HLHBC30	910079	440	HMMER 1.8	PFAM: C2 domain	PF00168	104.78	45	305
			blastx.2	1-phosphatidylinositol-	pir S14113 S14113	83%	6	332
				4,5-bisphosphate		74%	408	512
				phosphodiesterase 1				
HFBDJ13	1195217	131	blastx.14	SH3 domains-containing	pir T09071 T09071	%06	178	118
,				protein POSH - mouse		%95	1171	7
						76%	869	136
						39%	272	5

				57% 41% 28% 30%	898 514 823 315	699 370 939 600
	DEAR	M. CI13 J	0100010	701	100	383
441 HIMIMEK 2.1.1	FFA.	FFAM: SH3 domain	FF00018	/8.6	105	769
blastx.2 (,	AFC H3s	(AF030131) Plenty of SH3s; POSH [Mus	gb AAC40070.1	78%	3	473
442 HMMER 1	FAI oFAI	PFAM: Eukaryotic protein kinase domain	PF00069	114.02	72	353
stx.2	AL1	ypothetical	emb CAB55955.1	94%	6	353
<u>d</u>	rote	protein [Homo sapiens]		. 65%	350	622
-				63%	2	58
133 HMMER PF	À	PFAM: Eukaryotic protein	PF00069	53.16	95	292
ety 14		(AF144094)	01622468319bl A BOS	74507	350	017
Pi vice	יין זין	nal myosin-15	81/0224002/80/AAL 02 903 11	45%	128	240
	Hon			%99	800	880
				37%	72	152
				%95	87	134
				%08	96	125
				78%	28	207
-		-		37%	69	140
				21%	178	219
				767	216	287
		-		46%	354	398
	İ			33%	339	401

						30%	66	197
						20%	452	487
	911357	443	HMMER	PFAM: Src homology	PF00018	14.09	989	853
HWWDN3 4			1.8	domain 3		-		
			blastx.2	(AF053130)	gb AAC40124.1	42%	56	874
	-			unconventional myosin		%99	788	898
				MYO15 [Mus musculus]				
HCEPW85	911374	135	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	83.52	3	260
	· · · · · ·		blastx.14	predicted using	gi 3875903 emb CAA	87%	3	260
				Genefinder; Similarity to 1 1 cDNA	94127.1	,		
HMTAW8	1071602	136	blastx.14	(AF230904) c-Cbl-	gi 7188749 gb AAF37	94%	-	354
3				interacting protein [Homo	854.1 AF230904_1	48%	7	168
						21%	88	210
						%65	7	87
						61%	298	351
			·			75%	425	460
						62%	425	448
HMTAW8	911385	444	HMMER 1.8	PFAM: Src homology domain 3	PF00018	76.18	1	159
•			blastx.2	(AF230904) c-Cbl-	gb AAF37854.1 AF2	94%	1	354
				interacting protein [Homo	30904_1	52%	7	210
			-	sapiens]	I	48%	7	168
						61%	298	351
						75%	425	460
HDMAV01	911386	445	HMMER 1.8	PFAM: Src homology domain 3	PF00018	52.13	264	413

blastx.2	unnamed protein product	emb CAB42388.1	73%	Ξ,	410
HAMAED	+	pro0010	%00I		116
1.8	domain 3	PF00018	47.19	293	460
blastx.2	(AF104246) enhancer of filamentation 1 homolog	gb AAD11795.1	48%	281	553
	[Gallus gallus]				
HMMER	R PFAM: Src homology	PF00018	80.7	277	444
blastx.14	+-	gil167839 oh AAA33	470%	777	135
	[Dictyostelium discoideum]	229.1)
HMMER	 	PF00022	141.45	125	469
			,	· <u>-</u>	
blastx.2	ACTIN-LIKE-7-BETA.	sp Q9Y614 Q9Y614	72%	2	580
blastx,14		gi 508701 gb AAC49	52%	192	854
	neoformans	074.1	48%	932	129
			30%	837	1 086
LLJ	HMMER PFAM: Actins	PF00022	262.03	134	703
blastx.2	actin 1 - Trypanosoma	pir A27724 A27724	53%	134	715
	brucei		39%	718	963
			40%	942	102
HMMER	PFAM: Actin	PF00022	345.2	170	109
- 1	+				9
blastx.2	actin - Phaffia rhodozyma	pir S70377 S70377	40%	2	109

HTEJT86	1090517	143	blastx.14	actin [Diphyllobothrium	gi 1098579 gb AAA8	20%	142	684
	v			dendriticum]	2604.1	52%	029	
		:				55%	22	6
								129
HTEJT86	911626	448	HMMER 2.1.1	PFAM: Actin	PF00022	106.8	4	366
			blastx.2	ACTIN.	sp Q9UVF3 Q9UVF3	44%	25	369
						%99	366	410
HTEMA54	1134919	144	blastx.14	(AF113526) actin-like-7-	gi 5524058 gb AAD4	94%	55	135
			,	alpha [Homo sapiens]	4109.1 AF113526_1			6
ITTENANCA	911666	449	HMMER	PFAM: Actin	PF00022	320.7	247	116
HIEMA34			7.1.1					-
			blastx.2	ACTIN-LIKE-7-ALPHA.	sp Q9Y615 Q9Y615	95%	55	116
						82%	1121	7
-								136
								0
HTLGJ17	1135518	145	blastx.14	(AF191277) cytoplasmic	gi 6478616 gb AAF13	%65	360	440
				actin [Cavia porcellus]	923.1 AF191277_1	44%	521	574
HTLGJ17	915136	450	HMMER	PFAM: Actins	PF00022	25.12	237	317
			1.8			-		
			blastx.2	DJ63M2.2 (similar to	sp CAC08484 CAC0	81%	93	413
				ACTIN) (Fragment).	8484	%92	403	465
HOUES64	918119	146	HMMER	PFAM: Aldehyde	PF00171	138.5	3	278
			2.1.1	dehydrogenase family				
		:	blastx.2	lactaldehyde	pir A38165 A38165	%86	3	275
			``	dehydrogenase (EC				
				1.2.1.22) aldA -				
				Escherichia coli				
HMSCD15	982250	147	blastx.14	FBP 17 [Mus musculus]	gi 1255033 gb AAC5	93%	453	635

	APPAPA DA CONTROL DE LA CONTRO				2479.1			
HMSCD15	918133	451	HMMER 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
			blastx.2	(AK000975) unnamed	dbj BAA91451.1	%86 .	453	635
				protein product [Homo		78%	387	479
				sapiens]		28%	80	175
НБQБХ20	919027	452	HMMER 2.1.1	PFAM: PX domain	PF00787	73.4	246	695
	٠		blastx.14	serine/threonine protein	gi 294637 gb AAA42	78%	633	974
				kinase [Rattus norvegicus]	137.1	44%	465	578
HLTHP86	1110457	149	blastx.14	(AF161420) HSPC302	gi 6841254 gb AAF28	95%	498	134
				[Homo sapiens]	980.1 AF161420_1	%92	1351	6
					•	100%	1811	183
	-					52%	1295	3
								184
,								6
								135
HLTHP86	919354	453	HMMER 2.1.1	PFAM: TBC domain	PF00566	69.4	855	127
			blastx.2	(AF161420) HSPC302	gb AAF28980.1 AF1	%68	456	135
	-			[Homo sapiens]	61420_1	%66	1309	2
						52%	1253	197
								4
								130
HMSOL52	921126	454	HMMER 1.8	PFAM: EF hand	PF00036	12.43	276	359
			blastx.2	CG11041 PROTEIN.	9Z8\6\0 9Z8\6\0 ds	45%	102	464
	921782	455	HMMER	PFAM: Eukaryotic protein	PF00069	83.68	4	564

HAHGD33			1.8	kinase domain				
			blastx.14	(AF145690)	gi 5052670 gb AAD3	%89	-	297
				BcDNA.LD28657	8665.1 AF145690_1	26%	412	609
-				[Drosophila melanogaster]		%09	304	426
						39%	929	804
	921783	152	HMMER	PFAM: Eukaryotic protein	PF00069	58.81	507	797
ННЕНС53			1.8	kinase domain				
			blastx.14	(AF145690)	gi 5052670 gb AAD3	%6L	292	803
				BcDNA.LD28657 [Drosophila melanogaster]	8665.1 AF145690_1	70%	321	563
HE2PB01	921850	456	HMMER	PFAM: Actin	PF00022	35.9	29	616
			2.1.1					
			blastx.2	HSPC281 (Fragment).	sp AAF28959 AAF28 959	100%	2,	541
HOUDP52	1219522	154	blastx.14	CG7846 PROTEIN.	60XA6Dl60XA6Dlds	43%	27	491
						52%	1218	136
						35%	501	-
•						35%	1002	752
						,		120
			·					2
HOUDP52	922102	457	HMMER 2.1.1	PFAM: Actin	PF00022	32	092	109
			blastx.2	CG7846 PROTEIN.	60XV69 Q9VX09 qs	36%	208	110
						46%	23	4
								190
HHGAE47	1127881	155	blastx.14	(AF187305) calmodulin [Myxine glutinosa]	gi 5932428 gb AAD5 6955 1 AF187305 1	45%	59	499
	922194	458	HMMER	PFAM: EF hand	PF00036	16.77	171	257
HHGAE47			1.8				•	

			blastx.2	calmodulin [validated] -	pir S48728 MCHU	48%	310	576
HMCGL45	1165349	156	blastx.14	(AF187305) calmodulin	gi 5932428 gb AAD5 6955 11 A F 1 8 7 3 0 5 1	45%	464	904
HMCGL45	922195	459	HMMER 2.1.1	PFAM: EF hand	PF00036	26.6	460	546
			blastx.2	CALMODULIN.	sp Q9U6D3 Q9U6D3	45%	460	867
HELEF11	1153884	157	blastx.14	gamma-glutamyl	gi 1552811 gb AAB0	100%	1283	531
				phosphate reductase [Escherichia coli]	8663.1			
HELEF11	926930	460	HMMER	PFAM: Pyridoxal-	PF00282	202.9	146	565
			2.1.1	dependent decarboxylase	-			
				conserved domain	-			
			blastx.2	glutamate decarboxylase	pir B43332 B43332	81%	131	721
				(EC 4.1.1.15) beta -		100%	45	152
				Escherichia coli		%95	595	780
						47%	564	620
HETJX04	1212235	158	blastx.14	GRANUPHILIN-A.	sp Q9R0Q1 Q9R0Q1	%46	9	683
						64%	685	810
			-			87%	804	827
HETJX04	927120	461	HMMER 2.1.1	PFAM: C2 domain	PF00168	150.4	6	260
			blastx.2	GRANUPHILIN-A.	sp Q9R0Q1 Q9R0Q1	94%	9	683
		•	•			21%	685	831
				1		48%	719	859
HSOBC04	927280	462	HMMER 2.1.1	PFAM: EF hand	PF00036	23.5	278	346
			blastx.2	hypothetical protein DKFZp586I0821.1 -	pir T42709 T42709	%88	41	388

				human (fragment)				
HE8PW83	0866901	160	blastx.14	(AB002584) beta-alanine- pyruvate aminotransferase 1	gi 1944136 dbj BAA1 9549.1	%98	4	546
HE8PW83	927532	463	HMMER 1.8	PFAM: Aminotransferases class- III pyridoxal-phosphate	PF00202	139.27	4	465
			blastx.2	ALANINE GLYOXYLATE AMINOTRANSFERASE 2 PRECURSOR (EC 1 1	sp Q64565 AGT2_R AT	83%	4	546
HWLEA48	927676	161	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	32.82	190	381
			blastx.2	(AF169034) protein kinase [Homo sapiens]	gb AAF12757.2 AF1 69034_1	59% 100% 51%	154 89 287	429 166 415
HNHNP81	1129143	162	blastx.14	(AF091575) olfactory receptor [Rattus norvegicus]	gi 3769641 gb AAC6 4595.1	62% 61% 72%	618 236 502	896 505 621
HNHNP81	928378	464	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	58.09	233	511
			blastx.2	OLFACTORY RECEPTOR (FRAGMENT).	sp Q9Z231 Q9Z231	61% 52%	236 502	505 618
HFIDL68	1123641	£91	blastx.14	G protein-coupled receptor [Lymnaea stagnalis]	gi 438129 emb CAA8 0651.1	44%	945 1086	742
HFIDL68	928475	465	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin	PF00001	50.42	∞	319

	397	154	433		499	233		395	761	848	110	0	163	7	230	6	170	635	247	_	109	4	611	9	461	872	118
	8	1277	359		90	3	-	n	489	89/	1023		1320	2124	675 2	462	2328		1101 2	354		1125					
	0					80		\ <u> </u>																			
	38%	100%	11.52		29%	50.8		85%	64%	85%	38%		38%	40%	99%	31%	27%	23%	40%	30%	20%	25%					
																			~								
	$^{\prime}\mathrm{BP0}$	AD4		7.117.7	× × 4			A41	,				136		-												
	sp Q9VBP0 Q9VBP0	gi 5360127 gb AAD4	1001		splQ9V W49 Q9V W4 9			gi 205278 gb AAA41					pir H83136 H83136														
	∂9VBI	36012	PF00036	11100	% ^6^	PF00069		05278	=======================================				H8313			-											
) ds	Slig 280	PF(1)ds	-		gil	562.1			-	pir														
		EN-60	CIII		•	PFAM: Eukaryotic protein		ciated	Si					t073	[imported] - Pseudomonas	aeruginosa (strain PAO1)											
	CG5042 PROTEIN	(AF155116) NY-REN-60	and	ומחשל	CG8334 PROTEIN (FRAGMENT).	ıryotic	Ξ	male germ cell-associated	kinase (mak) [Rattus				ehyde	dehydrogenase PA4073	Pseudo	strain F											
(.	42 PR((2116) (Hon	PFAM: EF hand	7	CG8334 PRO (FRAGMENT	f: Euke	kinase domain	germ ce	(mak)	gicus			probable aldehyde	rogena	rted] -	nosa (s	•										
family)	CG50	(AF15	PFAM	600	CG83	PFAN	kinase	male g	kinase	norvegicus			probal	dehyd	[impo	aerugi	•		•								
	ε.2	ç.14	IER	,	7:3	1ER		ς.14					٤.14							•							
	blastx.2	blastx.14	HMMER	∞. 	blastx.2	HMMER	2.1.1	blastx.14					blastx.14														
		164	466			165							166														
		61				<u>ش</u>							19	_													
		1925911	929264			932583							1226719														
		<u> 7</u> 05	HUJCT05			(005		-				3H58						_	_	_	_	_				-
		HUJCŤ05	HUJ				HTEGO05						HRDBH58														

			1 2 3 1 2 3		3	
29%	29% 34% 44 44 100% 100%	29% 34% 96% 100% 100% 58% 66%	29% 34% 34% 100% 100% 58% 66% 66% 52% 33% 57% 52%	29% 34% 34% 100% 100% 58% 66% 66% 52% 33% 52% 52% 98%	29% 34% 34% 100% 100% 130.82 52% 52% 33% 52% 52% 82.59	29% 34% 34% 100% 100% 66% 66% 66% 52% 33% 52% 33% 82.59 82.59
Octobrilact corrigid						
dehydrog	ИЕR х.14	MER x.14 x.14 MER	x.14 x.14 x.14 x.14	MER x.14 x.14 x.14 x.14	x. 14 x. 14 x. 14 MER MER	x. 14 X. 14 X. 14 X. 14 X. 14 X. 14
	167 HMIN 2.1.1 blastx					
· .		4	4		4	
						HSDGW22 HNTMD79 I HNTMD79 HCE5J51 9

					-	42%	630	743
						31%	186	299
						46%	267	605
ннег042	934527	470	HMMER 2.1.1	PFAM: C2 domain	PF00168	128.8	203	472
			blastx.14	(AB025258) granuphilin-a	gi 5926736 dbj BAA8	40%	128	505
				[Mus musculus]	4656.1	21%	887	105
					-	46%	695	7
						39%	707	892
						31%	263	820
						46%	644	376
						38%	572	682
				•		75%	107	610
								130
HLQDC55	1082368	171	blastx.14	(AK002037) unnamed	gi 7023676 dbj BAA9	46%	332	496
				protein product [Homo	2048.1	45%	149	253
				sapiens				
HLQDC55	934528	471	HMMER 2.1.1	PFAM: C2 domain	PF00168	81.1	1	216
	•	j	blastx.2	CG15078 PROTEIN.	sp Q9V8M4 Q9V8M	34%	7	441
					4	43%		234
						64%	444	494
HFPHI62	1195825	172	blastx.14	rabphilin-3A - bovine	pir A48097 A48097	%56	184	1111
						%89	4	6
HFPHI62	934529	472	HMMER 1.8	PFAM: C2 domain	PF00168	106.44	27	293
			blastx.2	rabphilin-3A - mouse	pir JX0338 JX0338	%06	3	410
HE8QH09	1152238	173	blastx.14	(AB000893)	gi 1840399 dbj BAA1	%56	28	591
				synaptotagmin 3 [Mus	9204.1	%96	585	923

				musculus]		39%	46	228
						33%	193	351
						39%	453	521
НЕ8ОН09	934532	473	HMMER 2.1.1	PFAM: C2 domain	PF00168	168.2	77	337
			blastx.14	(AB000893)	gi 1840399 dbj BAA1	95%	56	568
				synaptotagmin 3. [Mus	9204.1	%86	564	830
				musculus]		42%	407	556
						33%	573	731
						32%	170	328
,						34%	99	205
			٠			100%	21	53
						39%	430	498
HFAAX29	1128791	174	blastx.14	(AF000423)	gi 2130632 gb AAB5	%66	25	570
				synaptotagmin XI [Rattus	8344.1	35%	385	510
				norvegicus]		25%	169	333
						47%	331	387
HFAAX29	934540	474	HMMER 2.1.1	PFAM: C2 domain	PF00168	115.2	194	463
			blastx.2	SYNAPTOTAGMIN XI.	sp O08835 O08835	%86	8	550
						32%	149	490
HHFOC79	1182276	175	blastx.14	(AF081251) putative eps	gi 3415099 gb AAC3	%26	84	296
				norvegicus]	1.775.1			-
HHFOC79	935406	475	HMMER	PFAM: EF hand	PF00036	13.96	186	263
			blastx.2	EH domain containing 2.	sp AAF40470 AAF40 470	%86	54	248
HOGEQ43	935465	476	HMMER 1.8	PFAM: Src homology domain 3	PF00018	28.13	28	132
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	T	Τ							Г				Γ.		Г			, 				1		1			_
132	433	370			571	574	484	409	996	561	720	363	779		977			286	120	9		422		428			
37	567	810	335	765	744	747	687	537	745	361	209	313	315		324			14	1153			210		3			_
93%	53.7	93%	%06	29%	35%	30%	27%	27%	20%	38%	52%	52%	31.25		45%			29%	%19			17.62		53%			
gb AAD19748.1	PF00431	pir 152657 152657					•		gi 7106102 emb CAB	76028.1			PF00069		emb CAB76028.1			gi 3004482 emb CAA	71076.1			PF00083		emb CAA71076.1			
(AF132480) Ese2 protein [Mus musculus]	PFAM: CUB domain	seizure-related protein	SEZ-6 precursor - mouse						(AL157917) similarity to	endopeptidases 1			PFAM: Eukaryotic protein	kinase domain	(AL157917) similarity to	endopeptidases	[Schizosaccharomyces 1	putative integral	membrane transport	protein [Rattus	norvegicus]	PFAM: Sugar (and other)	transporters	putative integral	membrane transport	protein [Rattus	[0.000000000000000000000000000000000000
blastx.2	HMMER 2.1.1	blastx.2							blastx.14			`	HMMER	1.8	blastx.2	•		blastx.14				HMMER	1.8	blastx.2			
	177					_			178				477					179				478					
	938398								1178621				940369				-	1156432				941348					
	нсес023								HTGAU79					HTGAU79				HE9F133				HE9F133					

	941862	480	HMMER	PFAM: 7 transmembrane	PF00001	118.47	2	029
HNHCP79			1.8	receptor (rhodopsin family)			•	
			blastx.14	(AF102533) olfactory	gi 3983394 gb AAD1	25%	2	658
				receptor F7 [Mus musculus]	3325.1			, •
HTLIY52	1194806	181	blastx.14	TESTIS-SPECIFIC	sp Q61241 Q61241	46%	624	956
				SERINE/THREONINE		48%	126	398
				KINASE.		45%	411	563
						42%	549	605
HTLIY52	942161	481	HMMER	PFAM: Eukaryotic protein	PF00069	251.19	166	. 933
			1.8	Kinase domain				
	-		blastx.2	serine/threonine kinase [Mus musculus]	gb AAA99535.1	44%	133	936
	942527	182	HMMER	PFAM: Eukaryotic protein	PF00069	9.65	406	612
HRAED74			1.8	kinase domain				-
,			blastx.2	(AB023658)	dbj BAA75246.1	%16	71	346
				Ca/calmodulin-dependent		81%	388	648
				protein kinase kinase		71%	342	425
				alpha, CaM-kinase kinase		%88	662	889
				alpha [Rattus norvegicus]		,		
	943757	183	HMMER	PFAM: 7 transmembrane	PF00001	80.79	274	573
HFKKN77			1.8	receptor (rhodopsin				
				family)				
			blastx.2	G-protein coupled	pir JC7289 JC7289	82%	160	714
				receptor, SREB3 - human				
HTEMU66	1205381	184	blastx.14	MEK KINASE ALPHA.	119960 119960 ds	51%	714	962
						%99	633	899
HTEMU66	944419	482	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	114.85	613	963

			blastx.2	MEK Kinase 3 [Mus	gb AAB03535.1	49%	604	948
				musculus]	-	29%	209	340
HWAGU62	1206797	185	blastx.14	Zinc transporter like 1.	sp AAF43422 AAF43	%56	264	827
					422	%96	696	151
			-			93%	29	_
						33%	22	262
								111
	945368	483	HMMER	PFAM: Cation efflux	PF01545	152	619	139
HWAGU62			2.1.1	family		-		5
			blastx.2	(AC007231) putative	gb AAD32753.1 AC0	45%	388	858
				cation transport protein	07231_1	45%	910	138
				[Arabidopsis thaliana]		38%	883	9
	_							951
HFPFB39	1198036	186	blastx.14	CG8745 PROTEIN.	26UV99 Q9VU95	%59	153	614
					-	%09	693	935
				٠		92%	945	111
		-				%99	1332	∞
						35%	1161	141
						%05	609	7
		,						132
								∞
								989
HFPFB39	946170	484	HMMER	PFAM:	PF00202	235.05	1613	714
		•	1.8	Aminotransferases class-				
				III pyridoxal-phosphate	,			
	,		blastx.2	hypothetical protein	pir T25848 T25848	46%	1613	651
		-		T01B11.2 -			-	•
				Caenorhabditis elegans				
HPMFI38	1165993	187	blastx.14	(AB005451) RST [Mus musculus]	gi 2696709 dbj BAA2 3875.11	51%	30	296
				an an an an an an an an an an an an an a			100	2

860 564	15 488		125 604	125 643 610 921	325 738				0/ 0/0											
32.16	43%	 	406.7	90%	62%	47%	52%	7%)	- 2//7	36%	36%	36% 33% 64	36% 33% 64 64 47%	36% 33% 64 47% 34%	36% 33% 64 47% 34%	36% 33% 64 47% 34%	36% 33% 64 47% 34% 33%	36% 33% 64 47% 34% 33% 33%	36% 33% 64 64 47% 34% 33% 33% 33%	36% 33% 64 47% 34% 33% 34% 38% 47%
PF00083	emb CAB09724.1		PF01284	pir JH0300 JH0300	gi 1018989 dbj BAA2	0476.1						PF00084	PF00084 splO02839 O02839	PF00084 sp O02839 O02839 emb CAA90392.1	PF00084 sp O02839 O02839 emb CAA90392.1	PF00084 sp O02839 O02839 emb CAA90392.1 PF00084	PF00084 sp O02839 O02839 emb CAA90392.1 PF00084 sp Q28797 Q28797	PF00084 sp O02839 O02839 emb CAA90392.1 PF00084 sp Q28797 Q28797	PF00084 sp 002839 002839 emb CAA90392.1 PF00084 sp Q28797 Q28797	PF00084 sp O02839 O02839 emb CAA90392.1 PF00084 sp Q28797 Q28797
ar (and other)	renal organic anion	[Pseudopleuronectes americanus]	PFAM: Synaptophysin / synaptoporin	synaptoporin - rat	porcine membrane	cofactor protein [Sus	scrofa]					PFAM: Sushi domain (SCR reneat)	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader [Rattus norvegicus]	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader [Rattus norvegicus] PFAM: Sushi domain (SCR repeat)	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader [Rattus norvegicus] PFAM: Sushi domain (SCR repeat)	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader [Rattus norvegicus] PFAM: Sushi domain (SCR repeat) UNKNOWN PROTEIN (FRAGMENT).	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader [Rattus norvegicus] PFAM: Sushi domain (SCR repeat) UNKNOWN PROTEIN (FRAGMENT).	PFAM: Sushi domain (SCR repeat) PORCINE MEMBRANE COFACTOR PROTEIN. C4BP beta chain, leader [Rattus norvegicus] PFAM: Sushi domain (SCR repeat) UNKNOWN PROTEIN (FRAGMENT).
HMMER	stx.2		HMMER 2.1.1	x.2	blastx.14				_			MER		MER x.2 x.2	MER x.2 x.2	MER MER MER	MER X.2 X.2 X.2 X.2 X.2 X.2 X.2 X.2	MER x.2 x.2 MER x.2	MER x.2 x.2 MER x.2	MER x.2 x.2 MER x.2
485			188		189		,					486	486	486	486	190	190	190	486	190
946252			946830	-	1152417					_		947973	947973	947973	947973	947973 1091087 947999	947973	947973 1091087 947999	947973	947973
HPMFI38			HBXDJ07		HOFMS43				,			HOFMS43	HOFMS43	HOFMS43 HOVC014	HOFMS43 HOVCO14	HOFMS43 HOVC014	HOFMS43 HOVC014 HOVC014	HOFMS43 HOVC014 HOVC014	HOFMS43 HOVCO14 HOVCO14	HOFMS43 HOVC014 HOVC014

				phosphodiesterase 1				
HTEPE35	948475	488	HMMER	PFAM:	PF00387	163.8	839	507
			2.1.1	Phosphatidylinositol-				
	-			specific phospholipase C,				
				Y domain				
			blastx.2	1-phosphatidylinositol-	pir S14113 S14113	48%	839	06
				4,5-bisphosphate				
				phosphodiesterase 1				
HE8UA52	1229490	192	blastx.14	collagen alpha 3(VI) chain	pir A37797 A37797	34%	121	729
				precursor - chicken		32%	805	135
						35%	700	3
					-	19%	208	819
						44%	814	330
						24%	196	298
					-	20%	808	306
						26%	208	861
						30%	395	330
								484
HE8UA52	948509	489	HMMER 1.8	PFAM: von Willebrand factor type A domain	PF00092	57.11	208	561
			blastx.2	collagen alpha 3(VI) chain - mouse (fragment)	pir S32605 S32605	41%	121	576
HOUBE50	1090776	193	blastx.14	neuroligin 3 [Rattus	gi 1145791 gb AAA9	74%	376	114
				norvegicus]	7871.1	%29	31	0
				r		77%	277	252
						%89	1134	381
								118
HOUBE50	948519	490	HMMER 1.8	PFAM: Carboxylesterases	PF00135	55.97	16	243

			blastx.2	Neuroligin 3 isoform HNL3s (Fragment).	sp AAF71231 AAF71 231	%02	31	243
HAJAV28	1165229	194	blastx.14	(AK000544) unnamed	gi 7020711 dbj BAA9	%56	96	111
				protein product [Homo	1243.1	100%	1064	∞
				sapiens]	-		•	134
HAJAV28	948630	491	HMMER 2.1.1	PFAM: Actin	PF00022	35.9	120	230
			blastx.2	Uncharacterized hypothalamus protein HARP11.	sp AAF67655 AAF67 655	97%	96	458
HAQBZ89	1083554	195	blastx.14	strong similarity to class-	gi 1707274 gb AAB3	49%	249	578
				III of 1 elegans]	7999.1	38%	594	881
						52%	873	992
						54%		72
						28%	186	221
	949061	492	HMMER	PFAM:	PF00202	65.49	89	325
HAQBZ89			1.8	Aminotransferases class-	-			
			blacty 2	CG8745 DROTEIN	2011/10Cl3011/10Clas	/003	c	71,
HELHF07	949067	196	HMMER	PFAM:	PF00207	38 85	0,50	205
			1.8	Aminotransferases class-				
				III pyridoxal-phosphate	-			
			blastx.14	4-aminobutyrate	gi 1742132 dbj BAA1	85%	83	295
				aminotransferase (EC	4871.1	95%	21	86
		,		2.6.1,19) 1 1		45%	246	311
				aminotransferase).		100%	_	18
				[Escherichia coli]		•		
HE9QQ22	1127726	197	blastx.14	(AB002584) beta-alanine-	gi 1944136 dbj BAA1	77%	92	418
				pyruvate aminotransferase	9549.1	%08	418	585

						85%	587	628
						100%	677	269
HE9QQ22	080646	493	HMMER	PFAM:	PF00202	105.1	285	545
			2.1.1	Aminotransferases class-				
				III pyridoxal-phosphate				•
			blastx.2	ALANINE	sp Q64565 AGT2_R	51%	. 3	107
				GLYOXYLATE	AT	43%	545	0
				AMINOTRANSFERASE		46%	682	100
				2 PRECURSOR (EC 1 1		•	•	3
						,		666
HSDSB06	949151	494	HMMER 2.1.1	PFAM: SH3 domain	PF00018	249.3	483	647
			blastx.2	(AL133047) hypothetical	emb CAB61374.1	%86	3	863
			-	protein [Homo sapiens]		30%	9	848
			-			33%	222	848
	949199	199	HMMER	PFAM: von Willebrand	PF00092	70.8	1461	117
HACAD35			2.1.1	factor type A domain				4
			blastx.2	SIMILAR TO COCH-	NGU9000009lds	%66	1464	952
				5B2.	0	100%	947	648
	,					95%	657	457
						22%	944	663
						20%	1005	952
HEQAP17	949358	200	HMMER	PFAM: 7 transmembrane	PF00001	94.57	741	436
			1.8	receptor (rhodopsin family)	:			
		,	blastx.2	Orphan seven-	sp AAF59827 AAF59	84%	786	295
				transmembrane receptor.	827			
	950884	495	HMMER	PFAM: EF hand	PF00036	15.74	285	202
HMTBB17			1.8					·
			blastx.2	CDNA FLJ10466 FIS,	sp BAA91628 BAA9	100%	513	100

				CLONE NT2RP1001665.	1628			
HKGDE58	945039	496	blastx.2	CDNA FLJ10466 FIS,	sp BAA91628 BAA9	%98	17	835
				CLONE NT2RP1001665.	1628	30%	281	691
						55%	169	825
	,					36%	069	914
						35%	32	208
HKGDE58	588056	497	HMMER 1.8	PFAM: EF hand	PF00036	15.98	304	221
			blastx.14	(AJ133836) calmodulin 2	gi 4581211 emb CAB	28%	337	179
			-	Branchiostoma floridae	40132.1	37%	166	119
HCHMW4	1144323	203	blastx.14	calmodulin [Plasmodium	gi 385234 gb AAA29	%09	376	564
0				falciparum]	508.1	46%	136	348
					-	38%	349	573
						36%	157	345
						32%	481	564
HCHMW4 0	951518	498	HMMER. 2.1.1	PFAM: EF hand	PF00036	129.9	486	572
			blastx.2	Calmodulin-like skin protein.	sp AAF66821 AAF66 821	%86	135	572
HE8QZ34	1143411	204	blastx.14	predicted using	gi 3875264 emb CAB	39%	941	120
				Genefinder; similar to EF	01132.1	20%	437	_
				hand (2 domains)		40%	695	595
			,	[Caenorhabditis elegans]		32%	227	877
					-	76%	1082	412
								118
HE8QZ34	952283	499	HMMER 1.8	PFAM: EF hand	PF00036	12.97	543	617
			blastx.2	CG4662 PROTEIN.	sp Q9VDT8 Q9VDT8	38%	249	086

						42%	249	878
						33%	977	108
					,			4
HWAFG04	1227627	205	blastx.14	PRO1038.	sp AAF71042 AAF71	.26%	5	550
					042	44%	536	745
HWAFG04	952878	200	HMMER	PFAM: Eukaryotic protein kinase domain	PF00069	93.74	1655	945
			blastx.14	(AC002343) Ser/Thr	gi 2262107 gb AAB6	41%	1655	138
				protein kinase isolog	3615.1	48%	1319	33
				[Arabidopsis thaliana]		42%	1046	118
					-	75%	1355	2
								933
				;				133
								2
HTEKT33	953308	501	HMMER	PFAM: Eukaryotic protein	PF00069	200.58	428	139
			1.8	kinase domain				3
			blastx.2	(AC007661) putative	gb AAD32787.1 AC0	41%	722	100
				protein kinase	07661_24	36%	1070	6
				[Arabidopsis thaliana]	-	29%	428	124
								3
					:			628
HBXDM07	953622	502	HMMER 2.1.1	PFAM: Sec1 family	PF00995	2.96	267	575
			blastx.2	Vacuolar protein sorting	sp AAF91174 AAF91	83%	141	728
		-		33B.	174	%16	_	141
						35%	587	902
HFPFA83	955614	208	HMMER	PFAM: 7 transmembrane	PF00001	107.6	316	681
			1.8	receptor (rhodopsin family)				
			blastx.2	G-protein coupled	pir JC7289 JC7289	%86	202	735

				receptor, SREB3 - human				
HKADO36	956115	503	HMMER	PFAM: Sugar (and other)	PF00083	44.03	2	277
			1.8	transporters				
	965956	210	HMMER	PFAM: Sugar (and other)	PF00083	121.54	206	147
HFXKG51			1.8	transporters				
			blastx.2	No definition line found	gb AAB18499.1	100%	260	982
		,		[Escherichia coli]				
HFPHR82	957528	504	HMMER	PFAM: Actin	PF00022	91.7	1322	357
			2.1.1					
			blastx.2	Uncharacterized	sp AAF67655 AAF67	.100%	1523	273
				hypothalamus protein	655			
				HARP11.				
HISAF59	959140	212	HMMER	PFAM: Eukaryotic protein	PF00069	89.46	340	771
			1.8	kinase domain				
			blastx.14	(AC002343) Ser/Thr	gi 2262107 gb AAB6	39%	460	89/
				protein kinase isolog	3615.1	33%	397	468
				[Arabidopsis thaliana]				
НСЕНD66	1136122	213	blastx.14	neuronal calcium sensor	gi 498032 gb AAA88	·%86	2	562
				[Rattus norvegicus]	510.1			
	929160	505	HMMER	PFAM: EF hand	PF00036	64.2	311	397
HCEHD66			2.1.1					
			blastx.2	Neuronal calcium sensor-	sp AAD01642 AAD0	100%	14	583
				1.	1642	,		
HE8UY74	1163590	214	blastx.14	(AF080119) contains	gi 3600036 gb AAC3	38%	13	291
				similarity to protein	5524.1	%89	367	441
	•			kinase 1		61%	464	502
HE8UY74	960914	909	HMMER	PFAM: Eukaryotic protein	PF00069	36.37	114	407
			1.8	kinase domain				
			blastx.14	(AF080119) contains	gi 3600036 gb AAC3	36%	117	290
				The same of the sa				

_				similarity to protein	5524 11	45%	13	
				kinase 1	-	73%	366	410
						37%	467	553
HAHIY08	962113	215	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	74.92	68	278
			blastx.14	similar to tyrosine kinase	gi 470364 gb AAC47	44%	192	278
				[Caenorhabditis elegans]	047.1	64%	18	92
				,	-	58%	108	179
Н2СВН45	963811	507	HMMER 1.8	PFAM: Src homology domain 3	PF00018	13	194	310
			blastx.2	Kryn [Mus musculus]	dbj BAA19686.1	%58	2	373
				-		%62	381	467
						87%	460	483
					. ,	%0/	131	160
HMVAM0 9	963814	208	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.79	728	802
\ \			blastx.2	(AK001580) unnamed protein product [Homo sapiens]	dbj BAA91769.1	%96	20	802
HFPEN04	1199663	218	blastx.14	CG8745 PROTEIN.	sp Q9VU95 Q9VU95	%59	156	617
			,			%09	969	938
						%59	948	112
						%99	1335	
						35%	1164	141
						20%	612	2
					-			133
								1 689
HFPEN04	964824	509	HMMER	PFAM:	PF00202	33.54	259	489
		~						

			1.8	Aminotransferases class-				
				III pyridoxal-phosphate				
			blastx.2	CG8745 PROTEIN.	sp Q9VU95 Q9VU95	. 62%	148	492
HSLJD02	1104452	219	blastx.14	UhpC protein [Escherichia coli]	gi 148114 gb AAA24 722.1	. %56	145	927
HSLJD02	965826	510	HMMER 18	PFAM: Sugar (and other)	PF00083	19.53	464	874
			blastx.2	UhpC protein [Escherichia coli]	gb AAA24722.1	100%	56	907
HDPFZ30	1220164	220	blastx.14	Sulfate transporter.	sp CAC05432 CAC0	25%	1684	151
					5432	48%	1433	7
					-	32%	1154	133
						%05	180	5
				•		35%	1199	966
								139
								114
								0
HDPFZ30	966752	511	HMMER	PFAM: Sulfate transporter	PF00916	60.2	1496	123
			2.1.1	family				~
			blastx.2	(AF180728) sulfate	gb AAD53951.1	28%	175	807
				transporter [Drosophila		25%	7	196
				melanogaster				
HPJCR33	852996	512	HMMER 1.8	PFAM: C2 domain	PF00168	31.15	13	267
			blastx.2	E3 UBIQUITIN LIGASE SMURFI (FRAGMENT).	sp Q9UJT8 Q9UJT8	%68	7	375
	008996	513	HMMER	PFAM: Eukaryotic protein	PF00069	32.41	1020	1119
HIOAK34			1.8 Flooty 14	Kinase domain	011345247319hIA AC7	75%	954	110
			Ulasta. 14	(207400)	B107027103B011101			

				serine/threonine protein	1014.1			0
				kinase TAO1 [Rattus	-	ŕ		•
				norvegicus]				•
HE8NI24	971296	223	HMMER	PFAM: 7 transmembrane	PF00001	61.74	453	707
			1.8	receptor (rhodopsin	-			
				family)				
			blastx.2	G-protein coupled	pir T47131 T47131	93%	345	707
				receptor, SREB2 - human	,	%88	722	748
HAMFM39	1055532	224	blastx.14	(AK001509) unnamed	gi 7022807 dbj BAA9	53%	3860	343
				protein product [Homo	1729.1	100%	4171	2
				sapiens]				410
	971347	514	HMMER	PFAM: Src homology	PF00018	67.14	1136	130
HAMFM39			1.8	domain 3				9
-			blastx.2	(AK001509) unnamed	dbj BAA91729.1	%65	4511	401
				protein product [Homo			·	7
				sapiens]				
UCON CITE	971414	515	HMMER	PFAM: EF hand	PF00036	10.69	19	141
HBGMG39			1.8					
	.		blastx.2	45 KDA CALCIUM-	sp Q61112 CB45_M	94%	7	165
				BINDING PROTEIN	OUSE			
				PRECURSOR (STROMAL 1				
HSXBV89	1128699	226	blastx.2	TYPE I	sp Q9UJ47 Q9UJ47	93%	7	203
				TRANSMEMBRANE		73%	313	7
			٠	RECEPTOR		29%	742	104
				PRECURSOR.				4
								146
								4
	971821	516	HMMER	PFAM: Sushi domain	PF00084	43.6	123	290

HSXRV89			211	(SCR reneat)				
CO A CONTROLL			7:1:1	(Bell lepeut)			1	1
			blastx.2	TYPEI	sp Q9UJ47 Q9UJ47	85%	3	635
				TRANSMEMBRANE		32%	96	536
				RECEPTOR				-
				PRECURSOR.				
HBIOZ10	1143756	227.	blastx.14	(AF003134) strong	gi 2088685 gb AAB5	43%	3	497
				similarity to the	4139.1			
-				CDC2/CDX 1				
HBIOZ10	973131	213	HMMER	PFAM: Eukaryotic protein	PF00069	121.1	3	365
			1.8	kinase domain			•	
			blastx.2	(AF003134) strong	gb AAB54139.1	%09	3	305
		-		similarity to the			-	
				CDC2/CDX subfamily of	-			
				ser/thr protein kinases				
				[Caenorhabditis elegans]				
HTLEJII	1085651	228	blastx.14	(AF144573) Mx-	gi 4868443 gb AAD3	%69	35	268
-				interacting protein kinase	1319.1 AF144573_1	40%	437	592
				PKM [Mesocricetus		45%	293	397
				auratus]		38%	877	939
HTLEJ11	973302	518	HMMER	PFAM: Eukaryotic protein	PF00069	55.9	44	223
			2.1.1	kinase domain		-		
		,	blastx.14	(AF144573) Mx-	gi 4868443 gb AAD3	%69	35	268
				interacting protein kinase	1319.1 AF144573_1	40%	437	592
				PKM [Mesocricetus		45%	293	397
				auratus]		38%	877	939
HAWAM6	1207835	229	blastx.14	SPARC-RELATED	VW9Q9WVW9Qqq	63%	280	972
6				PROTEIN.	6N	53%	193	438
					-	23%	961	122
			,			52%	49	4
						48%	223	198

,						46%	640	333
						23%	382	756
						34%	343	624
			·			20%	604	411
						33%	160	657
						28%	1025	831
						38%	2238	112
								0
	·-							230
							-	0
HAWAM6 9	943104	519	blastx.2	SPARC-RELATED PROTEIN.	sp Q9WVN9 Q9WV	21%	31	261
73 4 4 / 11 4 11	973465	520	HMMER	PFAM: EF hand	PF00036	10.13	76	26
HAWAMO 9			×.					
			blastx.14	(AF070470) SPARC- related protein [Mus musculus]	gi 5305327 gb AAD4 1590.1 AF070470_1	62%	133	S
HSCKD11	1056288	230	blastx.14	(AJ243342) nicotinic	gi 6688136 emb CAB	%86	1292	183
				acetylcholine receptor	65091.1	%88	2347	
		,		alpha 9 subunit [Homo		100%	54	288
				sapiens]		33%	3000	9
						35%	2938	203
					٠			310
								298 8
	973894	521	HMMER	PFAM: Neurotransmitter-	PF00065	31.56	147	257
HSCKD11			1.8	gated ion-channel				
			blastx.2	(AJ243342) nicotinic	emb CAB65091.1	%06	120	296

		_						
				acetylcholine receptor				
				alpha 9 subunit [Homo				•
				sapiens]				
HDPLT62	973945	522	HMMER	PFAM: Neurotransmitter-	PF00065	102.12	417	746
		í	1.8	gated ion-channel				
			blastx	GABA receptor rho-3	dbj BAA09322.1	78%	414	797
				subunit precursor [Rattus		95%	262	411
				norvegicus]				
HTPFX16	974296	232	HMMER	PFAM: PMP-	PF00822	50.2	48	299
			2.1.1	22/EMP/MP20/Claudin				
				family				•
	_		blastx.2	CLAUDIN-18.	sp P56857 CLDI_MO	67%	39	359
					USE	44%	316	483
HE9NO66	1079624	233	blastx.14	(AB035267) Nck-	gi 6472874 dbj BAA8	82%	449	775
				interacting kinase-like	7066.1	94%	2	283
	,			embryo specific kinase		80%	748	066
				[Mus musculus]				
HE9NO66	974353	523	HMMER	PFAM: Eukaryotic protein	PF00069	121.6	473	757
	,		1.8	kinase domain		-		
			blastx.14	(AB020741) NIK-related	gi 6009519 dbj BAA8	73%	449	817
				kinase [Mus musculus]	4943.1	94%	2	283
						%62	748	066
HSDJI44	1154068	234	blastx.14	(AE000180) 7,8-	gi 1786991 gb AAC7	94%	803	184
				diaminopelargonic acid	3861.1	%86	1828	6
				synthetase [Escherichia	-			208
				coli]				∞
HSDJI44	974784	524	HMMER	PFAM:	PF00202	511.4	894	183
			2.1.1	Aminotransferases class-				2
			blocky 14	(AEOOO180) 7 8	1170000011114	, 800	i C	
			Ulastx.14	(AEUUU18U) /,8-	gi 1/86991 gb AAC/	99%	795	184

	_			diaminonelargonic acid	3861 11	1000%	1027	-
	,			synthetase [Escherichia				186
				COII				0
HFXDP53	578868	525	HMMER 1.8	PFAM: CUB domain	PF00431	11.77	. 21	77
HWADY66	734565	236	HMMER	PFAM: Eukaryotic protein	PF00069	28.82	-	174
			1.8	kinase domain				
HLDBC63	1144557	237	blastx.14	carnitine	gi 755646 gb AAC41	%66	3	629
				palmitoyltransferase I	748.1		,	
				LIUIIIO Sapielis				
HLDBC63	745061	526	HMMER	PFAM: Carnitate	PF00755	258.4	3	410
			2.1.1	acyltransferase				
HFIVB68	752981	527	HMMER	PFAM: C2 domain	PF00168	35.53	406	570
	,		1.8					
			blastx.2	hypothetical protein	pir T12449 T12449	93%	187	615
				DKFZp564E1616.1 -		%16	692	835
				human (fragments)		%26	588	692
						%96	104	184
						%89	3	107
						36%	573	899
						27%	406	543
						36%	397	465
						54%	125	157
HTLAC56	1181355	239.	blastx.14	carnitine	gi 755646 gb AAC41	54%	9	599
				palmitoyltransferase I	748.1		•	
				[Homo sapiens]			-	
HTLAC56	753093	528	HMMER	PFAM: Carnitate	PF00755	143.3	9	422
			2.1.1	acyltransferase		,		
HSSAD41	753094	240	HMMER	PFAM: Carnitate	PF00755	8.06	51	299
			2.1.1	acyltransferase				

PF00069 gi 6224868 gb AAF05 989.1 AF191838_1 PF00069	PF00069 gi 6224868 gb AAF05 989.1 AF191838_1 PF00069 gi 4092850 dbj BAA3	59 1868 gb AAF05 AF191838_1 59 1850 dbj BAA3	68 gb AAF05 2191838_1 0	gb AAF05 1838_1 dbj BAA3	gb AAF05 1838_1 dbj BAA3	AAF05 38_1 38_1 3 BAA3	AAF05 8_1 8_1 8010	F05 10 10 10 10 10 10 10 10 10 10 10 10 10	43	\sim \sim \sim \sim \sim \sim \sim	$\frac{1}{2}$	
PF00069 gi 6224868 gb 989.1 AF1918	00069 5224868 gb 9.1 AF1918: 00069	59 1868 gb AF1918 59 1850 dbj	68 gb 31918:						AAE	AAF0 18_1 BAA BAD AAD:	AAF0 38_1 88_1 R010 AAD3 573_1	AAF05 38_1 BAA3 BAA3 AAD3 573_1
PF00 gi 62 989.1 PF00	18 12 18 19	19 12 7 19 18 -	069 248 AI 069 	069 24868 AF19 069 92850	069 24868 AF19 069 069 1	069 24868 gb AF1918 069 92850 db .1 036	069 24868 gb /4 AF19183 069 92850 dbj .1 978010 Q9F	069 24868 gb AA AF191838_ 069 92850 dbj BA 11 036 9R010 Q9R0	069 24868 gb AAF AF191838_1 069 92850 dbj BA/ 1 036 9R010 Q9R01(68443 gb AAE 1 AF144573_	PF00069 gi 6224868 gb AAF0 989.1 AF191838_1 PF00069 gi 4092850 dbj BAA 6281.1 PF00036 gi 4868443 gb AAD. 1319.1 AF144573_1	069 24868 gb AAF0 AF191838_1 069 92850 dbj BAA .1 036 9R010 Q9R010 68443 gb AAD3 1 AF144573_1	PF00069 gi 6224868 gb AAF05 989.1 AF191838_1 PF00069 gi 4092850 dbj BAA3 6281.1 PF00036 sp Q9R010 Q9R010 gi 4868443 gb AAD3 1319.1 AF144573_1 PF00069
												
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			2.1.1	calcium binding domain				
			blastx.2	TUMOR RELATED PROTEIN	sp Q9UBG3 Q9UBG	70%	89	325
HTEKS20	1124378	247	blastx.14	calcineurin [Bos taurus]	gi 312969 emb CAA5 0659.1	77%	53	562
HTEKS20	846714	535	HMMER 2.1.1	PFAM: EF hand	PF00036	84.7	453	539
			blastx.2	calcineurin regulatory chain - human	pir A33391 A33391	77%	09	569
HE9TK49	856343	536	HMMER 1.8	PFAM: Ion transport proteins	PF00520	77.02	11	256
			blastx.2	(AB012043) NBR13	dbj BAA36409.1	95%	2	256
				[Homo sapiens]		%05	256	327
						37%	259	282
IICHA TOI	867209	537	HMMER	PFAM: EF hand	PF00036	24.01	1227	130
HCHAIUI			1.8					4
			blastx.2	AD 3 (FRAGMENT).	sp Q9UQ32 Q9UQ32	41%	795	140
						72%	14	6
						57%	472	367
						%62	375	783
								476
HCEEN06	1150867	250	blastx.14	(AB025258) granuphilin-a	gi 5926736 dbj BAA8	32%	296	490
				[Mus musculus]	4656.1	48%	548	652
						47%	242	298
						42%	152	229
HCEEN06	878658	538	HMMER 1.8	PFAM: C2 domain	PF00168	51.79	203	466
HDPKI83	883382	251	HMMER 1.8	PFAM: C2 domain	PF00168	13.47	530	601

			blastx.2	MUNC13-4 PROTEIN.	sp Q9R189 Q9R189	%9L	194	631
						%56	735	794
						%08	199	738
HSPBQ12	1152258	252	blastx.14	copine I [Homo sapiens]	gi 1791257 gb AAC1	73%	55	570
					5920.1	63%	570 ′	851
HSPBQ12	884004	539	HIMMER	PFAM: C2 domain	PF00168	42.06	352	624
or and and	2,000		1.0		1000			
HPCID/8	886915	253	HMMER 2.1.1	PFAM: Sulfate transporter family	PF00916	26.4	265	381
			blastx.2	(AF030880) pendrin	gb AAC51873.1	40%	25	375
				[Homo sapiens]		-		
	886936	254	HMMER	PFAM: Src homology	PF00018	12.87	430	546
HDTKQ14			1.8	domain 3				-
			blastx.2	(AL049683) hypothetical	emb CAB41255.1	100%	439	555
				protein [Homo sapiens]		%95	9/	291
HRACK83	888037	255	HMMER	PFAM: Eukaryotic protein	PF00069	48.4	211	423
			1.8	kinase domain				
HSIAO78	889498	540	HMMER 1.8	PFAM: EF hand	PF00036	16.91	389	463
			blastx.2	HYPOTHETICAL 22.5	sp 043745 043745	%16	38	622
				KDA PROTEIN.			_	
HWAGS73	894404	257	HMMER	PFAM: Eukaryotic protein	PF00069	64.17	4	273
			1.8	kinase domain				
	898203	258	HMMER	PFAM: Calsequestrin	PF01216	1001.1	52	122
HCMSL08			2.1.1					
	-		blastx.2	calsequestrin precursor,	pir A60424 A60424	%56	112	119
				fast skeletal muscle -				7
			·	human				
	921176	541	HMMER	PFAM: Calsequestrin	PF01216	697.4	1372	569

HCMSL08			2.1.1					
			blastx.14	calmitine; calsequestrine	gi 688292 gb AAB32	93%	1372	593
HLWFN63	1101533	259	blastx.14	(AL049683) hypothetical	gil4678753lemblCAB	45%	470	937
-				protein [Homo sapiens]	41255.1	75%	686	102
	908437	542	HMMER	PFAM: Src homology	PF00018	12.81	515	664
HLWFN63			1.8	domain 3				
	•		blastx.2	(AL049683) hypothetical	emb CAB41255.1	44%	464	102
	000040	5	any of art	protein [Homo sapiens]				4
HPWAY10	908549	543	HMMEK 2.1.1	PFAM: KRAB box	PF01352	156.3	206	394
			blastx.14	zinc finger protein 30	gi 456269 emb CAA8	%01	152	325
				[Mus musculus	2913.1	%19	326	454
				domesticus]				
НООБНІ	1153909	261	blastx.14	(AC007842) BC331191_1 [Homo saniens]	gi 5080758 gb AAD3 9268 114C007842 3	100%	57	335
·	908588	544	HMMER	PFAM: KRAB box	PF01352	169.7	241	429
HOUDH19			2.1.1	•				
			blastx.2	(AC007842) BC331191_1	gb AAD39268.1 AC0	91%	226	549
			-	[Homo sapiens]	07842_3			
HDPFF24	909232	545	HMMER	PFAM: KRAB box	PF01352	121.3	158	349
,			2.1.1					
			blastx.2	(AC007228) R31665_2	gb AAD23606.1 AC0	20%	158	457
				[AA 1-673] [Homo	07228_1			
HWI FH94	1152278	263	blacty 14	(AK000265) unnamed	mi/7020230ldbilB A A 0	710%	730	030
)) 		protein product [Homo	1041.11	53%	595	669
				sapiens	-	57%	335	397

HWLFH94	909682	546	HMMER 1.8	PFAM: Src homology domain 3	PF00018	58.42	308	463
			blastx.2	(AK000265) unnamed protein product [Homo saniens]	dbj BAA91041.1	40%	215	535
HWMBM1 3	1152283	264	blastx.14	(AK000265) unnamed protein product [Homo saniens]	gi 7020230 dbj BAA9 1041.1	56% 41%	153 345	296 545
HWMBM1	909683	547	HMMER 1.8	PFAM: Src homology domain 3	PF00018	59.64	126	281
		· · · · · · · · · · · · · · · · · · ·	blastx.2	Eps8 [Mus musculus]	gb AAA16358.1	35%	33	317
HFIUE75	1172525	265	blastx.14	(AB037134) IRE homolog 1 [Arabidopsis thaliana]	gi 6729348 dbj BAA8 9784.1	53% 40% 28%	868 1126 526	113 113 125 125
HFIUE75	909758	548	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	85.68	377	664
			blastx.14	(AD000092) hypothetical human serine-threonine protein kinase R31240_1 Homo sapiens]	gi 1905906 gb AAB5 1171.1	43% 46% 47%	362 632 724	634 715 774
HNTCP13	909770	549	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain (AC006530) unknown [Homo sapiens]	PF00069 gi 4809337 gb AAD3 0182.11AC006530-4	102.96	445	930
НВІВQ89	909782	550	HMMER 2.1.1	PFAM: SH3 domain	PF00018	49.7	212	376

			blastx.2	p115 [Homo sapiens]	emb CAA55394.1	41%	14	397
HWBEG18	862606	551	HMMER 2.1.1	PFAM: EF hand	PF00036	33.3	505	591
			blastx.2	TVATOR	NNU9Ql9NNU9Qlds	55%	103	684
				RASGRP.	6	71%	869	688
						48%	2	142
HTAHB43	1221956	569	blastx.14	PUTATIVE RASGAP-	sp 043374 043374	%66	153	217
				ACTIVATING-LIKE		100%	2174	4
				PROTEIN.		%26	42	235
						. 34%	45	9
						31%	429	164
		-		•		57%	1436	140
			٠					524
								147
					-			7
	909845	552	HMMER	PFAM: GTPase-activator	PF00616	61.3	519	731
HTAHB43			2.1.1	protein for Ras-like GTPase				
			blastx.2	PUTATIVE RASGAP-	sp 043374 043374	%16	39	860
		•		ACTIVATING-LIKE PROTEIN		100%	-	33
	909846	270	HMMER	PFAM: C2 domain	PF00168	41.14	46	189
HSYBX32	٠		1.8		,			
			blastx.2	PUTATIVE RASGAP-	sp 043374 043374	%86	49	228
				ACTIVATING-LIKE				
				PROTEIN.				
HCEHE35	909937	553	HMMER	PFAM: Eukaryotic protein	PF00069	30.78	210	347
			1.8	kinase domain				
			blastx.14	protein kinase PRK2	gi 914100 gb AAB33	%99	204	365
				[human, DX3 B-cell	346.1			

				myolomo on line				
				Peptide, 984 aa] [Homo				
;				sapiens]				
HFCBB56	1204971	272	blastx.14	inositol 1,4,5-	pir S62358 S62358	44%	280	387
				trisphosphate-binding		31%	439	612
				protein, 130K - rat		79%	869	744
HFCBB56	910073	554	HMMER	PFAM: EF hand	PF00036	23.95	431	514
			blastx.2	1-phosphatidylinositol-	pir S14113 S14113	36%	275	565
				4,5-bisphosphate				-
				phosphodiesterase 1				
HAMFL82	910074	273	HMMER 1.8	PFAM: C2 domain	PF00168	73.4	6	212
			blastx.2	PHOSPHOLIPASE C-L2.	sp Q9QYG1 Q9QYG 1	%16	3	317
HBXCM38	1174533	274	blastx.14	unnamed protein product	gi 6740727 emb CAB	%16	405	134
		-		[unidentified]	69447.1	87%	13	6
								396
HBXCM38	980016	555	HMMER 1.8	PFAM: Src homology domain 3	PF00018	55.89	1062	123
	-		blastx.2	unnamed protein product	emb CAB69447.1	95%	402	131
-				[unidentified]		87%	13	9
					-	77%	1295	396
		·						134
71 0.711 111	910123	275	HMMER 2 1 1	PFAM: Sushi domain	PF00084	744.9	197.	358
FILITONIO			2.1.1	(SCN Tepeal)				
	· -		blastx:2	complement receptor 1 -	pir 136936 136936	29%	710	160 1
				chimpanzee (fragment)	,	30%	1166	 o
						31%	818	192

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	163	9	276	4	151	3	192		263	7	263	2	163	9	303		260	5	192	_	303		562	192		316	3	316	n
1958	710	1163	1757	1766	911	1970	1754	1166	2378	20	1244	2210	2210	11	11	710	11	710	23	992	710	23	23	20	32	728	983	728	713
30%	28%	73%	73%	78%	31%	79%	27%	78%	30%	36%	29%.	79%	79%	32%	32%	32%	32%	32%	30%	30%	32%	73%	36%	33%	27%	29%	30%	78%	31%
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2657	860	518	713	713	701	113	113	2417	1811	2642	80	1244	701	95	2219	2681	2618	734	1109	80	2219	725	1721	113	725	1550	2474	1472	1424
32%	31%	30%	31%	33%	32%	32%	32%	31%	30%	32%	34%	32%	33%	31%	29%	31%	767	30%	31%	32%	31%	32%	25%	29%	31%	28%	76%	30%	27%
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124	9	111	7	111	4	574	574	298	n	224	.7	310	6	460	163	6	111	_	547	298	3	313	0	310	6	117	-	153	7
2474	1721	1.100	893	11	1721	2555	1721	182	1100	2549	1997	38	1241	626	734	1250	1250	38	95	95	734	1769	725	725	1799	1472	593	371	
25%	25%	27%	73%	35%	76%	27%	79%	33%	76%	73%	30%	30%	32%	30%	30%	25%	24%	30%	31%	31%	31%	76%	31%	31%	767	25%	30%	22%	
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								197		638	254	737	254	68	806	692	740	419	=	17	17	1100	=	617	365	1220			
								357.8		31%	28%	34%	28%	35%	32%	34%	30%	30%	32%	27%	27%	34%	28%	30%	37%	29%			
								PF00084		gb AAB36703.1										-		-		-					
								PFAM: Sushi domain	(SCR repeat)	furrowed [Drosophila	melanogaster]	1		,		,													
					-			HMMER	2.1.1	blastx.2									-		,							• ,	
								556															-						
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148	0	445	148	0	571	148	6	192	378	375	192	168	168	378	372	324	609	320	378	174		186	275	156	3	898	426	558
								10	202	202	,	13	10	205	223	253	550	273	346	10		10	201	898	422	31		322
								75%	%99	39%	39%	38%	39%	41%	38%	37%	%05	20%	54%	51.15		%LL	44%	. 100%	%86	87%		35.3
								gi 3702174 emb CAA	07416.1											PF00018		emb CAA07416.1		gi 6997272 gb AAD4	5919.2 AF162130_1			PF00595
								(AJ007012) Fish protein	[Mus musculus]					,						PFAM: Src homology	domain 3	(AJ007012) Fish protein	[Mus musculus]	(AF162130) MAGUK	protein TEM-61 [Homo	sapiens]		PFAM: PDZ domain (Also known as DHR or
								blastx.14												HMMER	1.8	blastx.2		blastx.14				HMMER 2.1.1
								276							_		•			257				277				558
			-					1153883												911263				1162680		_ -		911293
								HE6GF02						-						HE6GF02				HOUFT36				HOUFT36

				GLGF).				
		-	blastx.2	(AF162130) MAGUK	gb AAD45919.2 AF1	%16	196	846
				protein TEM-61 [Homo	62130_1	%86	23	193
				sapiens				
	911312	559	HMMER	PFAM: Eukaryotic protein	PF00069	105.85	10	318
HAGGF84			1.8	kinase domain				
٠.		-	blastx.14	calmodulin-dependent	gi 3241849 dbj BAA2	%88	10	363
		-, ·		protein kinase II-delta	8870.1	87%	366	413
	-			dash [Oryctolagus		100%	320	364
				cuniculus]				
HTTKP07	1119031	279	blastx.14	(AL049683) hypothetical	gi 4678753 emb CAB	63%	8	205
				protein [Homo sapiens]	41255.1	28%	263	451
HTTKP07	911390	995	HMMER	PFAM: Src homology	PF00018	15.82	47	196
			1.8	domain 3				
			blastx.2	(AL049683) hypothetical	emb CAB41255.1	21%	8	289
				protein [Homo sapiens]		26%	292	450
HE9SE62	911476	561	HMMER	PFAM: Src homology	PF00018	47.65	268	435
	,		1.8	domain 3				
			blastx.2	(AK000007) FLJ00007	dbj BAA92232.1	43%	4	435
		_		protein [Homo sapiens]		64%	877	927
HUJAD24	1162674	281	blastx.14	serine/threonine kinase	gi 2052191 emb CAB	34%	457	777
				[Rattus norvegicus]	06295.1	48%	363	512
	-	_				34%	797	876
						21%	285	362
						21%	141	233
,						72%	1679	173
						45%	6	7
						24%	75	71
						72%	229	224
						42%	180	261

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								236
HUJAD24	911498	562	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	34.73	6	215
			blastx.14	AMP-activated protein	gi 758783 gb AAA64	45%	336	467
		·-		kinase homolog [Homo	850.1	45%	123	215
				sapiens]		37%	267	338
		4				54%	211	243
						41%	45	95
HWLFG75	1228123	782	blastx.14	DJ63M2.4 (novel protein).	sp CAC08483 CAC0	81%	472	861
					8483	91%	862	107
				,		100%	1140	4
	,							116
								3
HWLFG75	916563	563	HMMER 2.1.1	PFAM: EF hand	PF00036	24.1	187	273
	,		blastx.2	DJ63M2.4 (novel protein).	sp CAC08483 CAC0	%68	720	105
					8483	75%	457	∞
						100%	. 1123	717
								114
HT3BG12	921593	564	HMMER	PFAM: Eukaryotic protein	PF00069	27.09	109	183
•			1.8	kinase domain				
			blastx.14	CYCLIN-DEPENDENT	gi 3715669 emb CAA	%58	-	246
				KINASE (CDK)8	03585.1			
				[unidentified]				
HTLJC71	922923	284	HMMER	PFAM: Src homology	PF00018	9.14	1152	134
			1.0	domain 3				0
			blastx.2	(AL133030) hypothetical	emb CAB61362.1	94%	m	135
				protein [Homo sapiens]			-	5
HCOMM0	1194701	285	blastx.14	epidermal growth factor	pir I38728 I38728	44%	455	721
		•						

5				receptor kinase substrate -		59%	188	370
				Ilulian		40% 23%	53	232
						36%	125	190
						63%	1080	
						,		2
НСОММ0	925952	265	HMMER 1.8	PFAM: Src homology domain 3	PF00018	59.48	178	342
5								
			blastx.2	epidermal growth factor	gb AAA62280.1	46%	445	840
				receptor kinase substrate		43%	115	435
				[Homo sapiens]		23%	43	222
HSLJE54	926924	999	HMMER	PFAM: Pyridoxal-	PF00282	35.8	342	536
	-	-	2.1.1	dependent decarboxylase		•		
				conserved domain				
			blastx.2	CYSTEINE SULFINIC	srnn60 srnn60 ds	%86	198	548
				ACID		92%	542	739
				DECARBOXYLASE-		85%	721	885
			,	RELATED PROTEIN 4.		100%	885	806
HTGED07	927411	287	HMMER 2.1.1	PFAM: Sec1 family	PF00995	128.9.	34	297
			blastx.2	VESICLE TRANSPORT- RFI ATED PROTFIN	sp Q9Y6A8 Q9Y6A8	%68	25	309
	928365	288	HMMER	PFAM: 7 transmembrane	PF00001	24.58	6	248
HOFNH30			1.8	receptor (rhodopsin	-		·	
				family)				
			blastx.2	CALCIUM.	sp Q9UBY5 Q9UBY	75%	18	263
			•	MOBILIZING	Ş.	54%	265	375
				L YSOPHOSPHATIDIC				
				ו ייטו ושטעיו חוטע				

7 289			blastx.14	GOK [Homo sapiens]	gi 2264346 gb AAC5 1627.1	65%	10	951
928789 567 HMMER 1.8		HMN 1.8	1ER	PFAM: EF hand	PF00036	12.55	18	101
blastx.2	blastx.2	blastx.2		GOK.	sp Q13586 Q13586	%09	. 6	129 2
929193 290 HMMER 1.8		HMMER 1.8		PFAM: Src homology domain 3	PF00018	12.52	691	810
blastx.2	blastx.2	blastx.2		(AL049683) hypothetical	emb CAB41255.1	%69	145	102
				protein [Homo sapiens]	-	53%	945	102
931154 291 HMMER		HMMER		PFAM: 7 transmembrane	PF00001	53.4	2	262
2.1.1	2.1.1	2.1.1		receptor (rhodopsin family)				
blastx.2			, –	7 transmembrane G- protein coupled receptor.	sp AAG09275 AAG0 9275	75%	2	391
1052857 292 blastx.14 (blastx.14	 	1 -	(AF096300) HPK/GCK- like kinase HGK [Homo	gi 4322936 gb AAD1 6137.11	72%	2	412
				sapiens]				
932068 568 HMMER 2 1 1		HMMER		PFAM: Eukaryotic protein	PF00069	26.6	136	231
blastx.14	blastx.14	blastx.14		(AF096300) HPK/GCK-	gi 4322936 gb AAD1	63%	91	456
				like kinase HGK [Homo	6137.1	72%	09	158
				sapiens]		25%	232	312
1165420 293 blastx.14		blastx.14		(AF037261) SH3-	gi 3004948 gb AAC0	20%	517	909
				containing adaptor	9244.1	41%	625	969
				molecule-1 [Homo		40%	396	470
				sapiens		36%	141	215

нне буз	932851	695	HMMER	PFAM: Src homology	PF00018	30.41	526	708
			1.8	domain 3				
ННҒЈН79	933308	025	HMMER	PFAM: von Willebrand	PF00092	12.76	62	232
			1.8	factor type A domain		,		
	,		blastx.2	R31181_2, PARTIAL	sp 095783 095783	%66	14	316
				PROTEIN		-		_
			:	(FRAGMENT).				
HUCOW17	1155190	562	blastx.2	RHOGAP PROTEIN.	\$6860 \$6860 ds	61%	4	441
						62%	787	786
	933357	571	HMMER	PFAM: Src homology	PF00018	20.28	647	739
HUCOW17			1.8	domain 3				
	,		blastx.2	Graf protein [Homo	emb CAA71414.2	%19	1	261
				sapiens]		20%	809	751
						83%	756	608
					-	40%	187	246
HFKIT06	934019	572	HMMER	PFAM: Eukaryotic protein	PF00069	34.65	160	270
			1.8	kinase domain				
			blastx.14	p58 galactosyltransferase-	pir A38282 A38282	21%	178	270
				associated protein kinase -		40%	74	118
		-		human				
HDTBY88	1104159	297	blastx.14	(AF130372) serine-	gi 7108631 gb AAF36	%18	186	491
			,	threonine protein kinase 1	509.1 AF130372_1	%86	3	170
						100%	497	535
	934472	573	HMMER	PFAM: Eukaryotic protein	69000dd	93.6	3	302
HDTBY88			2.1.1	kinase domain				
			blastx.14	p56 KKIAMRE protein	gi 1517820 gb AAC5	82%	3	170
				kinase [Homo sapiens]	0918.1	35%	192	458
						100%	492	509
HWLHS82	1082268	298	blastx.2	(AC005581) R31237_1,	gb AAC33487.1	93%	162	905

				partial CDS [Homo		%88	1049	123
				sapiens		100%	96	7
								170
C6011 1/1111.	934505	574	HMMER	PFAM: Eukaryotic protein	PF00069	147.2	2	319
HWLHS82			7.1.1	kinase domain	-			
			blastx.2	(AC005581) R31237_1,	gb AAC33487.1	%06	89	364
				partial CDS [Homo		100%	2	92
				sapiens		40%	306	422
HDPNC96	1081629	299	blastx.14	HUMAN NDR [unidentified]	gi 2304746 emb CAA 03387.1	95%	3	734
	934520	575	HMMER	PFAM: Eukaryotic protein	PF00069	206.63	3	734
HDPNC96			1.8	kinase domain				
			blastx.14	HUMAN NDR	gi 2304746 emb CAA	95%	3	734
				[unidentified]	03387.1			
HCESI78	1197899	300	blastx.14	rabphilin-3A - bovine	pir A48097 A48097	%56	161	112
						%89	Ξ	9
								97
HCE5I78	934531	576	HMMER 1.8	PFAM: C2 domain	PF00168	49.14	213	413
			blastx.2	rabphilin-3A - bovine	pir A48097 A48097	83%	135	404
	,					61%	3	41
HISDS62	1159625	301	blastx.14	(AJ250425) Collybistin I [Rattus norvegicus]	gi 6706318 emb CAB 65966.1	%06	185	892
HISDS62	935932	277	HMMER 2.1.1	PFAM: RhoGEF domain	PF00621	51.3	229	486
		i	blastx.2	(AJ250425) Collybistin I [Rattus norvegicus]	emb CAB65966.1	%96	· —	483
69ЛОООН	937850	578	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	212.5	89	598

			blastx.2	(AF169035) protein	gb AAF12758.1 AF1	%86	89	829
				kinase [Homo sapiens]	69035_1			
HEMBT61	939957	303	HMMER	PFAM: Eukaryotic protein kinase domain	PF00069	9.92	16	285
			blastx.2	(AD000092) hypothetical	gb AAB51171.1	71%	13	441
				human serine-threonine	-			
				protein kinase R31240_1				
				[Homo sapiens]				
HRODZ70	1088554	304	blastx.2	kinase like protein	emb CAB10257.1	39%	254	544
				[Arabidopsis thaliana]		%05	524	109
	942673	085	HMMER	PFAM: Eukaryotic protein	PF00069	78.2	33	248
HRODZ70			2.1.1	kinase domain				
			blastx.2	kinase like protein	emb CAB10257.1	39%	33	323
				[Arabidopsis thaliana]		20%	303	380
	944057	581	HMMER	PFAM: Eukaryotic protein	PF00069	83.4	133	474
HHERQ79			1.8	kinase domain	-	ŭ		
			blastx.2	(AB016589) inducible	dbj BAA85154.1	%06	109	471
				IKappaB kinase [Mus				
				musculus]				
НСЕСМ90	945088	582	HMMER	PFAM: Src homology	PF00018	53.06	392	568
	945692	583	HMMER	PFAM: ATP P2X recentor	PF00864	438 5	247	855
HWHGW7			2.1.1				: . !)
2							;	
٠			blastx.2	(AF190822) P2X2A	gb AAF19170.1 AF1	%16	190	939
				receptor [Homo sapiens]	90822_1			
HPCRV84	1219890	308	blastx.14	MATERNAL	sp Q61846 Q61846	%46	138	839
				EMBRYONIC LEUCINE		·		
			,	ZIPPER KINASE				

	384	483	915	155	4	449		553			292		124	4	532	138		150	0	137	~	147	9	+71
-	157	127	757	4		21		1287			1287		516	101	1232	1408	1244	1411	1200	1143	383	597		_
	75.57	78%	149	82%		%88		214.2			100%		94%	%26	%06	100%	37%	40%	40%	%09	33%	33%		
	PF00069	dbj BAA11492.1	PF00018	gb AAD34595.1 AF1	46277_1	gi 4960047 gb AAD3	4595.1 AF146277_1	PF00001			sp AAF87078 AAF87	078	gi 5052319 gb AAD3	8501.1[AF118838_1									-	
(SEMINE I TINE CIVILINE I	PFAM: Eukaryotic protein kinase domain	similar to protein kinase of X.laevis, has putative 1	PFAM: SH3 domain	(AF146277) adapter	protein CMS [Homo sapiens]	(AF146277) adapter	protein CMS [Homo sapiens]	PFAM: 7 transmembrane	receptor (rhodopsin	family)	G-protein coupled	receptor HL WAR77.	(AF118838) citrin; adult-	onset type II citrullinemia	protein [Homo sapiens]									
	HMMER 1.8	blastx.2	HMMER	blastx.2		blastx.14		HMMER	1.8		blastx.2		blastx.14					-						
	585		309			586		310					311.									_		
	945856		946988			972348		947484					1127477											
	HPCRV84		HNS A 238			HNSAA28			HLWAR77				HTTJW49			,								

								4
•	•							117
		_						7
		-						481
								695
HTTJW49	948107	587	HMMER	PFAM: EF hand	PF00036	11.98	283	348
<u> </u>			1.8					
_			blastx.2	CITRIN.	sp Q9UNI7 Q9UNI7	84%	94	627
HWAFS18	1155193	312	blastx.14	(AF156884) RIP-like	gi 5059425 gb AAD3	%68	165	171
				kinase [Homo sapiens]	9005.1 AF156884_1			8
	948434	889	HMMER	PFAM: Eukaryotic protein	PF00069	115.98	225	632
HWAFS18			1.8	kinase domain				
			blastx.14	(AF156884) RIP-like	gi 5059425 gb AAD3	91%	165	632
				kinase [Homo sapiens]	9005.1 AF156884_1	%99	702	773
						100%	632	661
HFCBA44	1082762	313	blastx.14	(AB010633)	gi 2810987 dbj BAA2	61%	184	639
				carboxylesterase precursor [Macaca fascicularis]	4523.1			
HFCBA44	948533	589	HMMER	PFAM: Carboxylesterases	PF00135	34.24	315	485
			1.8	•				
			blastx.2	thiolesterase B (EC 3)	pir A47162 A47162	%95	2	208
		,		precursor - mallard		%09	423	482
						48%	184	264
HVADT77	1180374	314	blastx.14	alpha-3 collagen type VI	gi 211622 gb AAA03	25%	12	119
				[Gallus gallus]	201.1			
	948886	290	HMMER	PFAM: Kunitz/Bovine	PF00014	74.41	169	321
HVADT77			8.1	pancreatic trypsin		-	-	-
				minottor domain				
			blastx.2	alpha-3 collagen type VI	gb AAA03201.1	43%	130	330

	_			[Gallus gallus]				
HUFCN91	1189013	315	blastx.14	copine I [Homo sapiens]	gi 1791257 gb A·AC1	54%	103	540
				•	5920.1	48%	199	782
					•	71%	874	936
						75%	540	587
	,					64%	783	833
HUFCN91	949137	591	HMMER 1.8	PFAM: von Willebrand factor type A domain	PF00092	9.83	529	729
			blastx.14	copine I [Homo sapiens]	gi 1791257 gb AAC1	26%	103	588
-					5920.1	48%	971	133
						48%	562	3
						21%	1332	783
					-	45%	668	143
						64%	784	0
				-				100
								6
						i		834
	951351	316	HMMER	PFAM: PMP-	PF00822	182.3	3	476
HAGBX32			2.1.1	22/EMP/MP20/Claudin family			- , -	
			blastx.2	VOLTAGE-	sp O60359 CCG3_H	%68	12	551
				DEPENDENT	UMAN			
				CALCIUM CHANNEL				
	955336	593	HMMER	PFAM: Eukaryotic protein	PF00069	122.85	1458	934
HWMIB81			1.8	kinase domain				
-			blastx.2	(AK000528) unnamed	dbj BAA91232.1	100%	3	572
				protein product [Homo				
				sapiens				
HCEMU86	1156430	318	blastx.14	p87=transporter-like	gi 259174 gb AAB24	816	10	795

		173	788		338		332		332			886	118	3	593	851	736	439	993		727		103
		2124	3		42		72		36			527	974	444	732	713		182	931		959		47
		24.49	%66		93%		89.99		92%			20%	44%	20%	30%	75%		31.12	4.41		26		%96
028.1		PF00083	gb AAB24028.1	• • ·	gi 5915662 gb AAD5	1919.2 AF137378_1	PF00092		gb AAD51919.2 AF1	37378_1		sp AAF71042 AAF71	042		-			PF00069	PF00168		PF00036		sp AAG09692 AAG0 9692
protein cattle, Peptide,	742 aa] [Bos taurus]	PFAM: Sugar (and other) transporters	p87=transporter-like	protein [cattle, Peptide, 742 aal [Bos taurus]	(AF137378) integrin alpha	11 subunit precursor [Homo sapiens]	PFAM: von Willebrand	ractor type A domain	(AF137378) integrin alpha	11 subunit precursor	[Homo sapiens]	PRO1038.						PFAM: Eukaryotic protein kinase domain	PFAM: C2 domain		PFAM: EF hand		Reticulocabin precursor.
		HMMER 1.8	blastx.2		blastx.14		HMMER	1.8	blastx.2			blastx.14						HMMER 1.8	HMMER	1.8	HMMER	2:1::	blastx.2
		594			319		595					320						597	865		322		
		956864			1153911		957143					1204719			_			959020	961074		963290		
		HCEMU86			HRDAF83		HPDAF63	CO.TWOWILL				HUVGZ88						HUVGZ88	HSCKS55		HOEET48		`

15000011	964235	599	HMMER	PFAM: Mitochondrial	PF00153	235.26	995	183
HBODESI			1.8	carrier proteins				4
			blastx.14	aralar1 [Homo sapiens]	gi 3559910 emb CAA 74834.1	93%	20	205
HHFCK09	965304	324	HMMER 2.1.1	PFAM: TBC domain	PF00566	179.1	2305	165
			blastx.2	(AL022238) dJ1042K10.2	emb CAA18266.1	%16	2635	126
				(supported by		%86	1276	∞
				GENSCAN, FGENES and				389
				GENEWISE) [Homo sapiens]				
	905396	009	HMMER	PFAM: Src homology	PF00018	5.22	179	214
HC00Z11			1.8	domain 3				
			blastx.2	(AL022238) dJ1042K10.2	emb CAA18266.1	100%	182	589
				(supported by				
				GENSCAN, FGENES and				
			-	GENEWISE) [Homo				
HDPP035	1119032	326	blastx.14	(AL049683) hypothetical	gil4678753 emblCAB	63%	561	758
				protein [Homo sapiens]	41255.1	65%	816	086
						71%	84	146
						%59	300	359
						45%	1080	113
						25%	117	6
		·						245
HDPPO35	966248	601	HMMER 1.8	PFAM: Src homology domain 3	PF00018	14.07	009	749
				(41 040/003/1	1 0 4 0 4 10	200	3];
			blastx.2	(ALU49683) hypothetical protein [Homo sapiens]	emb CAB41255.1	39%	84	8 8
	209896	602	HMMER	PFAM: Actin	PF00022	291.1	77	111

HLWDZ53	:		2.1.1					
			blastx.2	Actin-related protein 3-	sp AAC98904 AAC9	%66	95	112
				beta.	8904	100%	54	986
HEOPL36	968826	603	HMMER 1.8	PFAM: Src homology domain 3	PF00018	79.81	316	483
			blastx.2	(AL049758) dJ437M21.3 (protein kinase C and	emb CAB51395.1	%66	178	486
				casein kinase substrate in				
				neurons 2) [Homo sapiens]				
HMCFS02	1152252	329	blastx.14	(AK000482) unnamed	gi 7020600 dbj BAA9	%65	72	725
				protein product [Homo sapiens]	1194.1	40%	716	781
HMCFS02	969326	604	HMMER 1.8	PFAM: C2 domain	PF00168	8.05	347	457
			blastx.2	CDNA FLJ20475 FIS, CLONE KAT07206.	sp BAA91194 BAA9 1194	29%	116	496
HDPSR15	999696	909	HMMER	PFAM: Eukaryotic protein kinase domain	PF00069	87.19	351	979
			blastx.2	(AB026289) protein	dbj BAA85045.1	%56	631	115
			• •	kinase SID6-1512 [Homo		%68	240	8
	971315	909	HMMER	PFAM: 7 transmembrane	PF00001	23.92	3	143
HNTAV78			1.8	receptor (rhodopsin family)				
			blastx.2	Cysteinyl leukotriene CysLT2 receptor.	sp BAB03601 BAB0 3601	100%	3	266
HFKDR14	1145842	332	blastx.14	(AF128625) CDC42-	gi 5006445 gb AAD3	%86	06	127

				binding protein kinase	7506.1 AF128625_1	100%	1279	7
				beta [Homo sapiens]				132
HFKDR14	974255	209	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	244.21	297	109
	<u></u>	· · · ·	blastx.2	(AF128625) CDC42-	gb AAD37506.1 AF1	%86	72	173
				binding protein kinase	28625_1	22%	1572	3
				beta [Homo sapiens]				170
HDPBI30	974711	333	HMMER	PFAM: 7 transmembrane	PF00001	171.31	386	109
	,		1.8	receptor (rhodopsin			·	9
				family)		•		
			blastx.2	G PROTEIN-COUPLED	NU69 8WNU69 ds	93%	206	131
				RECEPTOR.	W8			7
HODFF88	1094875	334	blastx.2	mixed-lineage protein	pir S32467 JU0229	73%	68	493
				kinase 1 - human		81%	763	696
HODFF88	974911	809	HMMER	PFAM: Eukaryotic protein	PF00069	101.43	86	370
		_	1.8	kinase domain				
			blastx.14	mixed-lineage protein	pir S32467 JU0229	74%	131	493
				kinase 1 - human		. 81%	763	921
						30%	751	915

- Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. The fifth column provides a description of the PFAM/NR hit identified by each analysis. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, score/percent identity, provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM"), as described below.
- The NR database, which comprises the NBRF PIR database, the NCBI GenPept [47] database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than 1.0e-07, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7. The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP

and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

- [48] The PFAM database, PFAM version 2.1, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, 1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., Durbin et al., Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFAM version 2.1. A HMM derived from PFAM version 2.1 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFAM family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFAM hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which show a significant match to a PFAM protein family.
- [49] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.
- [50] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling

immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

- Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).
- Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and having depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.
- [53] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

[54] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad.

Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation, therefor. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[55] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[56] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is

synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[57] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript and a primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase if used is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant gene.

- [58] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, and receiving ATCC designation numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, Table 6, or Table 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as described, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1Aor 2 by procedures hereinafter further described, and others apparent to those skilled in the art.
- [59] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.
- [60] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

- Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus 15:59-* (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res. 16:*9677-9686 (1988) and Mead, D. *et al.*, *Bio/Technology 9:* (1991).
- [62] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.
- Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by genes corresponding to SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.
- [64] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.
- [65] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often

advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

[67] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence The present invention also provides a polypeptide contained in Clone ID NO:Z. comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[68] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any

combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Further, representative examples of polynucleotides of the invention comprise, or [69] alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[70] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEO ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[71] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

- In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.
- [76] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent

hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[77] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[79] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization

conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[82] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next

sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[83] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the fourth column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

Clone ID NO: Z	SEQ ID NO: X	Contig ID:	EST Di Range of a	sclaimer Range of b	Accession #'s
HTPAD46	11	1048901	1 - 1561	15 - 1575	AW026547, AL119230, AI992054, AI968455, AW193784, AW193801, AA386091, AA386130, AI825443, AA004475, and Z79235.
HCWFF88	12	1092566	1 - 639	15 - 653	
HSSAX53	13	1198889	1 - 348	15 - 362	
НСЕРН71	14	522739	1 - 432	15 - 446	AA326209, AA383931, AL365319, and AL390715.
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НТТЕК47	16	1134534	1 - 1221	15 - 1235	AI651805, AI989837, AI718022, AA400005, AI458374, AA401437, AW205244, AA883445, AI478808, AW134723, AI689951, AI269389, AA865056, AI640798, H11911, R44433, AI688852, AI183700, AA424180, AI277599, R46805, and AA771819.
НТОВЕ75	17	1163883	1 - 1797	15 - 1811	AW192827, AA595431, AI251121, AI923335, AI284016, H30141, T70540, T90549, AI432106, AA953436, H27466, R50714, R50249, AI540363, T70809, AI659868, AW370667, Z99572, I36305, AL022146, M87861, M72332, M60235, L39075, M60230, M60228, M60231, M60229, M60232, M60227, and M60234.
HCFAT05	18	1156310	1 - 2145	15 - 2159	AL133816, AA811374, AI095381, M38217, M55515, L23499, M85217, X16001, M30312, M31744, AR050270, U38240, U38182, U96110, and U45979.
HFIAH37	19	1189001	1 - 1712	15 - 1726	AL134903, AI912243, AA976922, AI742663, AW028771, AW043595, AA478697, AA837145, W49831, AI354405, AA412384, AA602982, N62994, AA013476, AI674206, AA115419, AI377356, AW270325, AI479159, AA169423, AA133086, AA326624, H83962, R76363, AA587840, AI224540, H67227, H81547, AA665443, AA018206, AA662495, AW298791, AA251488, AA301274, AA132987, AI192416, AI300307, AA722928, AA478563, R76688, AA579347, AA501519, AA629042, AI299974, H70300, AI865166, AA252018, N79902, AI867958, AI300195, AA251195, AA251787, H65133, AW246148, AA644296, AA115418, AC004381, and AF227510.
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HFTDY67 25 1151220 1 - 1523 15 - 1537 Al335266, Al751901, Al751815, Al750604, Al040116, AW067945, AW239149, Al572373, Na2174, N22119, N71503, AF182316, AF182317, AB033033, AR018882, and AB026436. HYABL89 26 1090733 1 - 700 15 - 714 HCUEV29 27 1137791 1 - 703 15 - 717 Al570209, AA583494, AW337550, AW335428, Cl6961, AA878169, AW411072, AW16090, T24722, AA365566, AA365567, Al418046, AA350018, AW246233, and AL031283. HCESP56 28 1121751 1 - 506 15 - 520 AW247740, AW24709, AW204207, W39269, AA325536, R14422, W52568, Y16752, AL022170, and Z65186. HLQDT35 29 1154064 1 - 1308 15 - 1322 Al659435, AW06450, Al380742, Al953510, Al078578, AA707183, Al453381, Al445431, AW156858, AA871757, AW16880, AA131680, Al569636, Al140912, AA530976, AA410746, AA134742, AA152440, AA807317, AA283695, N66180, Al082380, Al269183, AA480063, AA635830, AA433870, Al631995, Al1637742, AA292134, AA131985, AA923686, Al580936, N30879, Al358610, AA1652441, AA253107, H92198, Al160395, AA830846, Al753274, AA253052, AA152441, AA85999, AA68100, AA165244, AA85995, R08557, R11497, AA358765, AA706241, AA134743, Al424722, Al800536, R08654, R10421, N99172, T89988, AA80424, W16996, Al934059, AA481922, AA292133, AA746933, N56752, AA290133, AA746933, N56752, AA290907, Al091625, and AL137699. HDPBS64 30 846624 1 - 743 15 - 757 AA888874, AA992389, and Al767840. HTBAB41 31 1052388 1 - 785 15 - 799 AA382198, H48825, H58945, and Al339780.	·					
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IIIIIII CE 52	75	1217026	1 2220	15 - 2242	and AR018882.
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HTPGG25	132	1217208	1 - 2771	13-2/83	A1973055, A1554720, A1768326,
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HOUES64	146	918119	1 - 304	15 - 318	1 1 2 1 5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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HSDGW22	167	934467	1 - 312	15 - 326	AF071071, AF170303, AF170304,
IISDGW22	107	334407	1 - 512	13 - 320	AF077658, and AF071070.
HNTMD79	168	1126594	1 - 649	15 - 663	AA305176.
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HE8QH09	173	1152238	1 - 1439	15 - 1453	D45858, D28512, and AB000893.
HFAAX29	174	1128791	1 - 842	15 - 856	AL119825, AW367632, AA333024, AA164770, N53725, AA984472, N44616, AF000423, AB026808, and D38522.
ННГОС79	175	1182276	1 - 2091	15 - 2105	W37105, W72587, AI417917, N40695, N40709, AI750977, AA399093, AA528204, AI160861, AI167229, W56631, AA845109, AA450162, AA740816, AA708621,

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HCECQ23	177	938398	1 - 796	15 - 810	AI480182, AI500178, AI873131,
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HTGAU79	178	1178621	1 - 1081	15 - 1095	AA579641, AI149891, AI028588,
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HE9FI33	179	1156432	1 - 1550	15 - 1564	AA010320, AA010384, and R01100.
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	101	1124000	1 - 1556	13-1332	AI827749, AI580407, AI819667, AI025487, AI223109, AI150036.
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	101	1154600	1 - 1556	13 - 1332	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322,
	101	1154000	1 - 1330	13-1332	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213,
	101	1194000	1 - 1330	13 - 1332	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857,
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HRAED74	182	942527	1 - 691	15 - 705	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and
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HRAED74 HFKKN77	182	942527	1 - 691	15 - 705	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658.
HRAED74	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658.
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039566, AL039678, AL039108,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039566, AL039678, AL039108, AL039538, AL039564, AL039509,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039566, AL039678, AL039108,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039538, AL039564, AL039509, D80253, AL039156, H00069, AL039128,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039566, AL039678, AL039108, AL039538, AL039564, AL039509, D80253, AL039156, H00069, AL039128, AL044407, AL036973, AL042909,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039566, AL039678, AL039108, AL039538, AL039564, AL039509, D80253, AL039156, H00069, AL039128, AL044407, AL036973, AL042909, AL045337, AL037051, AL045353,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL038837, AL039074, AL039566, AL039678, AL039108, AL039538, AL039564, AL039509, D80253, AL039156, H00069, AL039128, AL044407, AL036973, AL042909, AL045337, AL037051, AL045353, AL039423, D59787, AL039410,
HRAED74 HFKKN77	182	942527 943757	1 - 691 1 - 719	15 - 705 15 - 733	AI025487, AI223109, AI150036, AI024234, AW087713, T18864, AI479322, AA883975, AW341589, AA860213, AI831802, AA913074, AA608857, AI050685, AA860223, AA948538, and AI075930. AC005940, L42810, S83194, AF117384, and AB023658. AL039924, AL045794, AW013814, AL036630, T02921, AL044412, AL044364, T24119, T24112, AW450335, AL039476, D51250, AL039521, AL045341, AL039386, D80043, AL040992, AL039109, AL038531, AL037726, AL039629, AL039659, AL039625, AL039648, AL03837, AL039074, AL039566, AL039678, AL039108, AL039538, AL039564, AL039509, D80253, AL039156, H00069, AL039128, AL044407, AL036973, AL042909, AL045337, AL037051, AL045353, AL039423, D59787, AL039410, AL039150, AL038025, AL044530,
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HKGDE58	202	1129137	1 - 1325	15 - 1339	AW271462, AA582539, AI963340,
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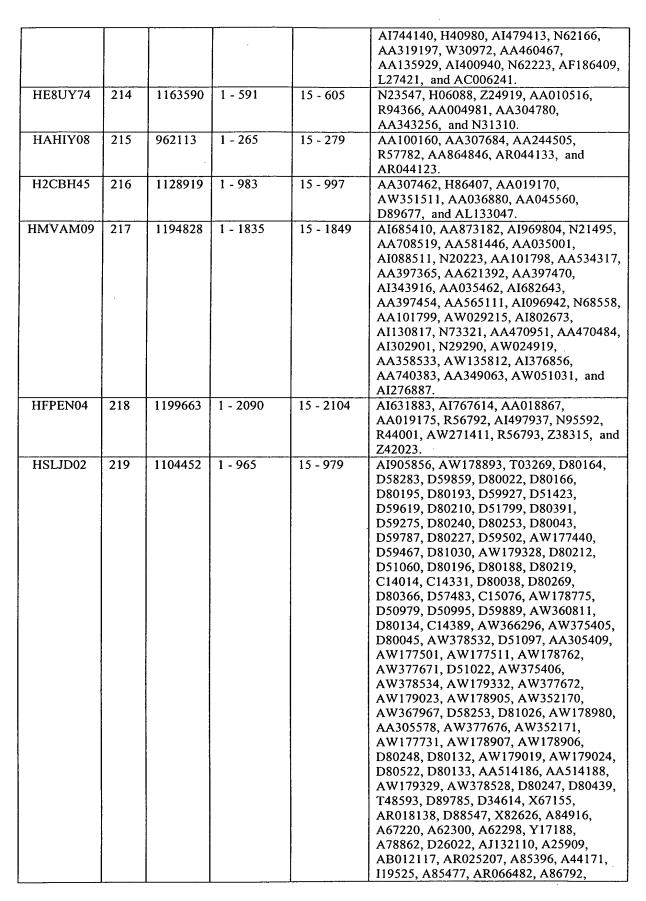
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HDPLT62	231	1027241	1 - 2693	15 - 2707	AI279417, AL079734, AA502991,
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1					AL078581, AL022311, AC005409,
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	1	1	}		AC007766, AC002364, AL035691,
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HTPFX16	232	974296	1 - 470	15 - 484	
HE9NO66	233	1079624	1 - 976	15 - 990	AI732997, AA865818, AA977633, Z69734,
ILLINOU	233	1077024	1-570	13 - 550	AB035267, AB020741, and Z68339.
HSDJI44	234	1154068	1 - 2093	15 - 2107	A38246, A11524, AR029497, E05333, and
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HFXDP53	235	1126294	1 - 1567	15 - 1581	AR001481.
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HWADY66	236	734565	1 - 490	13 - 304	AA923698, AI673803, AI302688,
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	1	ļ			H12318, R28631, A1638545, A1760745,
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HFIVB68	238	978211	1 - 823	15 - 837	AA332003, AB033033, AF182316,
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HTLAC56	239	1181355	1 - 836	15 - 850	AA614273, AA149526, AA722818,
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HSSAD41	240	753094	1 - 566	15 - 580	AA149526, AA151569, AA722818,
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HDAAV61	242	1188787	1 - 1319	15 - 1333	AA314786, AA160847, AA158845, AA157440, AA083972, AA159380,
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HDPKD75	243	1096253	1 - 623	15 - 637	AA923698, AL040000, Z21326,
HDI RD75	2 13	1000200	. 020		AR016417, AF191838, AF191839, and
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HTEON29	244	1126312	1 - 538	15 - 552	AW004028, AA432290, AI968030,
HILONZ	244	1120312	1 - 550	13 332	AW237673, AW138422, AA428635, and
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HCK A COA	245	1121800	1 - 497	15 - 511	AF170301, AF170302, AF077659, and
HSKAC24	245	1121800	1 - 497	13-311	AF144573.
	246	1016400	1 1701	16 1726	AW238721, AW265324, AW238371,
HTJAA71	246	1216498	1 - 1721	15 - 1735	AW238695, AW238323, AW084388,
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HTEKS20	247	1124378	1 - 1061	15 - 1075	AI936596, AA868353, AI797296,
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	1	Ì			AA431516, AA911681, AA781953,
	1				AI825106, AA298758, AI215028,
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НЕ9ТК49	248	1125192	1 - 1353	15 - 1367	AA086273, AF126965, AF126966,
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HCHAT01	249	1202275	1 - 2977	15 - 2991	AL079756, W80383, AA570709,
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	1	1		1	AA496647, R25017, AA348324, H46223,
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1			}		R08999, R09622, AW020710, and
	ļ	<u> </u>			AB014576.
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HSPBQ12	252	1152258	1 - 1130	15 - 1144	W02910, AA282287, N72351, AA829957,
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HPCID78	253	886915	1 - 793	15 - 807	
HDTKQ14	254	886936	1 - 541	15 - 555	AL023653, AL049683, AL359542,
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HRACK83	255	888037	1 - 566	15 - 580	AC005832.
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İ	1	1			AI565867, AI131012, AI144119, H65663,
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ļ	Ì	ļ			AA847967, AW027678, AL044698,
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		!			AW182206, AA011130, N78511,
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	1	İ			AC005183, AC005004, AC002541,
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		ļ			AC004129, AC004875, AL021877,
		1			AC006599, Z83822, AP000030, U61375,
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HLWFN63	259	1101533	1 - 3089	15 - 3103	AA707313, AI880426, AI684827,
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HUM ENOA	262	1152279	1 1260	15 1202	
HWLFH94	263	1152278	1 - 1268	15 - 1282	A1339104, AA861042, AA134985,
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AW378534, AW179332, AW377672,						AW378534, AW179332, AW377672,
AW179023, AW178905, D80132,				1	1	AW179023, AW178905, D80132,
AW360834, AA285331, D80439,			1			AW360834, AA285331, D80439,

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TABLE 4

Code	Description	Tissue	Organ	Cell Line	Disease	Vector
AR022	a_Heart	a_Heart				
AR023	a_Liver	a_Liver				
AR024	a mammary gland	a_mammary gland				
AR025	a Prostate	a Prostate				1
AR026	a small intestine	a small intestine			i	
AR027	a Stomach	a Stomach				
AR028	Blood B cells	Blood B cells				
AR029	Blood B cells activated	Blood B cells activated				
AR030	Blood B cells resting	Blood B cells resting				
AR031	Blood T cells activated	Blood T cells activated				
A B 022	Dia d'Esplia spatina					
AR032 AR033	Blood T cells resting	Blood T cells resting brain			 	
						
AR034	breast	breast	 		 	+
AR035	breast cancer Cell Line CAOV3	breast cancer	 			
AR036	cell line CAOV3	Cell Line CAOV3	 		<u> </u>	
AR037	L		ļ			
AR038	cell line transformed	cell line transformed				
AR039	colon	colon				
AR040	colon (9808co65R)	colon (9808co65R)				
AR041	colon (9809co15)	colon (9809co15)				
AR042	colon cancer	colon cancer	<u> </u>			ļ
AR043	colon cancer (9808co64R)	colon cancer (9808co64R)				
AR044	colon cancer 9809co14	colon cancer 9809co14				
AR045	corn clone 5	corn clone 5				
AR046	com clone 6	corn clone 6				
AR047	corn clone2	corn clone2				
AR048	corn clone3	corn clone3			L	L
AR049	Corn Clone4	Corn Clone4				<u> </u>
AR050	Donor II B Cells 24hrs	Donor II B Cells 24hrs				
AR051	Donor II B Cells 72hrs	Donor II B Cells 72hrs	-			
AR052	Donor II B-Cells 24 hrs.	Donor II B-Cells 24 hrs.				
AR053	Donor II B-Cells 72hrs	Donor II B-Cells 72hrs				
AR054	Donor II Resting B Cells	Donor II Resting B Cells				
AR055	Heart	Heart				
AR056	Human Lung (clonetech)	Human Lung (clonetech)				
AR057	Human Mammary (clontech)	Human Mammary (clontech)				
AR058	Human Thymus (clonetech)	Human Thymus (clonetech)				
AR059	Jurkat (unstimulated)	Jurkat (unstimulated)				
AR060	Kidney	Kidney			 -	+
AR061	Liver	Liver				
AR062	Liver (Clontech)	Liver (Clontech)				
AR063	Lymphocytes chronic	Lymphocytes			 	
WV003	Lymphocytes chronic	Lymphocytes	<u> </u>		<u> </u>	

	lymphocytic leukaemia	chronic lymphocytic				
AR064	Lymphocytes diffuse large	leukaemia Lymphocytes				
	B cell lymphoma	diffuse large B cell lymphoma				
AR065	Lymphocytes follicular lymphoma	Lymphocytes follicular lymphoma				
AR066	normal breast	normal breast				
AR067	Normal Ovarian (4004901)	Normal Ovarian (4004901)				
AR068	Normal Ovary 9508G045	Normal Ovary 9508G045	<u> </u>			
AR069	Normal Ovary 9701G208	Normal Ovary 9701G208				
AR070	Normal Ovary 9806G005	Normal Ovary 9806G005				
AR071	Ovarian Cancer	Ovarian Cancer				
AR072	Ovarian Cancer	Ovarian Cancer	 _		1	}
	(9702G001)	(9702G001)				
AR073	Ovarian Cancer (9707G029)	Ovarian Cancer (9707G029)				
AR074	Ovarian Cancer (9804G011)	Ovarian Cancer (9804G011)				
AR075	Ovarian Cancer (9806G019)	Ovarian Cancer (9806G019)				
AR076	Ovarian Cancer (9807G017)	Ovarian Cancer (9807G017)				
AR077	Ovarian Cancer (9809G001)	Ovarian Cancer (9809G001)				
AR078	ovarian cancer 15799	ovarian cancer 15799		· ·		
AR079	Ovarian Cancer 17717AID	Ovarian Cancer 17717AID				
AR080	Ovarian Cancer 4004664B1	Ovarian Cancer 4004664B1				
AR081	Ovarian Cancer 4005315A1	Ovarian Cancer 4005315A1				
AR082	ovarian cancer 94127303	ovarian cancer 94127303				
AR083	Ovarian Cancer 96069304	Ovarian Cancer 96069304		·		
AR084	Ovarian Cancer 9707G029	Ovarian Cancer 9707G029				
AR085	Ovarian Cancer 9807G045	Ovarian Cancer 9807G045				
AR086	ovarian cancer 9809G001	ovarian cancer 9809G001				
AR087	Ovarian Cancer 9905C032RC	Ovarian Cancer 9905C032RC				ļ
AR088	Ovarian cancer 9907 C00 3rd	Ovarian cancer 9907 C00 3rd				
AR089	Prostate	Prostate				ļ
AR090	Prostate (clonetech)	Prostate (clonetech)		ļ		ļ
AR091	prostate cancer	prostate cancer		<u> </u>	1	
AR092	prostate cancer #15176	prostate cancer #15176				
AR093	prostate cancer #15509	prostate cancer #15509			ļ	
AR094	prostate cancer #15673	prostate cancer #15673				
AR095	Small Intestine (Clontech)	Small Intestine (Clontech)				<u> </u>

AR096	Spleen	Spleen			
AR097	Thymus T cells activated	Thymus T cells			
,	11.,,,,,,,	activated			
AR098	Thymus T cells resting	Thymus T cells			
		resting			
AR099	Tonsil	Tonsil			
AR100	Tonsil geminal center	Tonsil geminal			ļ
	centroblast	center centroblast			
AR101	Tonsil germinal center B	Tonsil germinal		j	ļ
	cell	center B cell			
AR102	Tonsil lymph node	Tonsil lymph node			<u>-</u>
AR103	Tonsil memory B cell	Tonsil memory B cell			
AR104	Whole Brain	Whole Brain			
AR104 AR105	Xenograft ES-2	Xenograft ES-2			
AR106	Xenograft SW626	Xenograft SW626			
H0004	Human Adult Spleen	Human Adult	Spleen		Uni-ZAP XR
110004	Traman Addit Spicen	Spleen	op.cen		
H0008	Whole 6 Week Old				Uni-ZAP XR
	Embryo				
H0009	Human Fetal Brain				Uni-ZAP XR
H0011	Human Fetal Kidney	Human Fetal Kidney	Kidney		Uni-ZAP XR
H0012	Human Fetal Kidney	Human Fetal Kidney	Kidney		Uni-ZAP XR
H0013	Human 8 Week Whole	Human 8 Week Old	Embryo		Uni-ZAP XR
	Embryo	Embryo			
H0014	Human Gall Bladder	Human Gall Bladder	Gall Bladder		Uni-ZAP XR
H0015	Human Gall Bladder,	Human Gall Bladder	Gall Bladder		Uni-ZAP XR
	fraction II				
H0022	Jurkat Cells	Jurkat T-Cell Line			Lambda
		 			ZAP II Uni-ZAP XR
H0023	Human Fetal Lung	Ti Estati	7	-	Uni-ZAP XR
H0024	Human Fetal Lung III	Human Fetal Lung	Lung		Lambda
H0025	Human Adult Lymph Node	Human Adult Lymph Node	Lymph Node	ł	ZAP II
H0027	Human Ovarian Cancer	Lymph 140de		die	sease Uni-ZAP XR
H0027	Human Old Ovary	Human Old Ovary	Ovary	uis uis	pBluescript
H0028	Human Pancreas	Human Pancreas	Pancreas		Uni-ZAP XR
H0029	Human Placenta	Tunian Fancicas	Tancicas		Uni-ZAP XR
H0030	Human Placenta	Human Placenta	Placenta		Uni-ZAP XR
H0031	Human Prostate	Human Prostate	Prostate		Uni-ZAP XR
H0036	Human Adult Small	Human Adult Small	Small Int.		Uni-ZAP XR
110030	Intestine	Intestine	Cinan int.	[1
H0037	Human Adult Small	Human Adult Small	Small Int.		pBluescript
	Intestine	Intestine		L	
H0038	Human Testes	Human Testes	Testis		Uni-ZAP XR
H0039	Human Pancreas Tumor	Human Pancreas	Pancreas	dis	sease Uni-ZAP XR
		Tumor			
H0040	Human Testes Tumor	Human Testes	Testis	dis	sease Uni-ZAP XR
		Tumor		<u> </u>	
H0041	Human Fetal Bone	Human Fetal Bone	Bone		Uni-ZAP XR
H0042	Human Adult Pulmonary	Human Adult	Lung		Uni-ZAP XR
		Pulmonary	114	1:	sease Uni-ZAP XR
H0046	Human Endometrial	Human Endometrial	Uterus	118	sease Uni-ZAP XR
1100.40	Tumor	Tumor	 	 	Uni-ZAP XR
H0048	Human Pineal Gland	Human Pineal Gland	Licart		Uni-ZAP XR
H0050	Human Fetal Heart	Human Fetal Heart	Heart Brain	 	Uni-ZAP XR
H0051	Human Hippocampus	Human Hippocampus	Brain		Oili-ZAI AK
110053	Human Cerebellum	Human Cerebellum	Brain	 	Uni-ZAP XR
H0052	Human Cerebellum Human Umbilical Vein,	Human Umbilical	Umbilical		Uni-ZAP XR
	i ituman Ombincai vein.	i ituman Ombineal		1 1	1 0 Dr. AK
H0056	Endo. remake	Vein Endothelial	vein	l t	

H0057	Human Fetal Spleen					Uni-ZAP XR
H0059	Human Uterine Cancer	Human Uterine	Uterus		disease	Lambda
		Cancer				ZAP II
H0063	Human Thymus	Human Thymus	Thymus			Uni-ZAP XR
H0068	Human Skin Tumor	Human Skin Tumor	Skin	- <u>-</u>	disease	Uni-ZAP XR
H0069	Human Activated T-Cells	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0071	Human Infant Adrenal	Human Infant	Adrenal	}		.Uni-ZAP XR
11007#	Gland	Adrenal Gland	gland	GUL		Lini ZAD VD
H0075	Human Activated T-Cells (II)	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0081	Human Fetal Epithelium (Skin)	Human Fetal Skin	Skin			Uni-ZAP XR
H0083	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Jurkat Cells				Uni-ZAP XR
H0085	Human Colon	Human Colon				Lambda ZAP II
H0086	Human epithelioid	Epithelioid	Sk Muscle		disease	Uni-ZAP XR
	sarcoma	Sarcoma, muscle				<u> </u>
H0087	Human Thymus	Human Thymus		ļ		pBluescript
H0090	Human T-Cell Lymphoma	T-Cell Lymphoma	T-Cell		disease	Uni-ZAP XR
H0098	Human Adult Liver, subtracted	Human Adult Liver	Liver			Uni-ZAP XR
H0100	Human Whole Six Week Old Embryo	Human Whole Six Week Old Embryo	Embryo			Uni-ZAP XR
H0101	Human 7 Weeks Old Embryo, subtracted	Human Whole 7 Week Old Embryo	Embryo	 		Lambda ZAP II
H0102	Human Whole 6 Week	Human Whole Six	Embryo			pBluescript
	Old Embryo (II), subt	Week Old Embryo				'
H0105	Human Fetal Heart, subtracted	Human Fetal Heart	Heart			pBluescript
H0108	Human Adult Lymph Node, subtracted	Human Adult Lymph Node	Lymph Node			Uni-ZAP XR
H0116	Human Thymus Tumor, subtracted	Human Thymus Tumor	Thymus			pBluescript
H0118	Human Adult Kidney	Human Adult Kidney	Kidney			Uni-ZAP XR
H0122	Human Adult Skeletal Muscle	Human Skeletal Muscle	Sk Muscle			Uni-ZAP XR
H0123	Human Fetal Dura Mater	Human Fetal Dura Mater	Brain			Uni-ZAP XR
H0124	Human Rhabdomyosarcoma	Human Rhabdomyosarcoma	Sk Muscle		disease	Uni-ZAP XR
H0125	Cem cells cyclohexamide treated	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0130	LNCAP untreated	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0131	LNCAP + 0.3nM R1881	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0132	LNCAP + 30nM R1881	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
H0134	Raji Cells, cyclohexamide treated	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0135	Human Synovial Sarcoma	Human Synovial Sarcoma	Synovium			Uni-ZAP XR
H0136	Supt Cells, cyclohexamide treated	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		Uni-ZAP XR
H0141	Activated T-Cells, 12 hrs.	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0144	Nine Week Old Early Stage Human	9 Wk Old Early Stage Human	Embryo			Uni-ZAP XR
H0149	7 Week Old Early Stage Human, subtracted	Human Whole 7 Week Old Embryo	Embryo			Uni-ZAP XR

H0150	Human Epididymus	Epididymis	Testis	1		Uni-ZAP XR
H0154	Human Fibrosarcoma	Human Skin	Skin		disease	Uni-ZAP XR
H0156	Human Adrenal Gland	Fibrosarcoma Human Adrenal	Adrenal	 	disease	Uni-ZAP XR
	Tumor	Gland Tumor	Gland			
H0159	Activated T-Cells, 8 hrs., ligation 2	Activated T-Cells	Blood	Cell Line	,	Uni-ZAP XR
H0163	Human Synovium	Human Synovium	Synovium			Uni-ZAP XR
H0165	Human Prostate Cancer, Stage B2	Human Prostate Cancer, stage B2	Prostate		disease	Uni-ZAP XR
H0166	Human Prostate Cancer, Stage B2 fraction	Human Prostate Cancer, stage B2	Prostate		disease	Uni-ZAP XR
H0169	Human Prostate Cancer, Stage C fraction	Human Prostate Cancer, stage C	Prostate		disease	Uni-ZAP XR
H0170	12 Week Old Early Stage Human	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0171	12 Week Old Early Stage Human, II	Twelve Week Old Early Stage Human	Embryo			Uni-ZAP XR
H0172	Human Fetal Brain, random primed	Human Fetal Brain	Brain			Lambda ZAP II
H0175	H. Adult Spleen, ziplox					pSport1
H0176	CAMA1Ee Cell Line	CAMA1Ee Cell Line	Breast	Cell Line		Uni-ZAP XR
H0178	Human Fetal Brain	Human Fetal Brain	Brain			Uni-ZAP XR
H0179	Human Neutrophil	Human Neutrophil	Blood	Cell Line		Uni-ZAP XR
H0181	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0182	Human Primary Breast Cancer	Human Primary Breast Cancer	Breast		disease	Uni-ZAP XR
H0187	Resting T-Cell	T-Cells	Blood	Cell Line		Lambda ZAP II
H0188	Human Normal Breast	Human Normal Breast	Breast			Uni-ZAP XR
H0192	Cem Cells, cyclohexamide treated, subtra	Cyclohexamide Treated Cem, Jurkat,	Blood	Cell Line		Uni-ZAP XR
H0194	Human Cerebellum, subtracted	Raji, and Supt Human Cerebellum	Brain			pBluescript
H0196	Human Cardiomyopathy, subtracted	Human Cardiomyopathy	Heart		·	Uni-ZAP XR
H0201	Human Hippocampus, subtracted	Human Hippocampus	Brain			pBluescript
H0205	Human Colon Cancer, differential	Human Colon Cancer	Colon			pBluescript
H0208	Early Stage Human Lung, subtracted	Human Fetal Lung	Lung			pBluescript
H0212	Human Prostate, subtracted	Human Prostate	Prostate			pBluescript
H0213	Human Pituitary, subtracted	Human Pituitary				Uni-ZAP XR
H0214	Raji cells, cyclohexamide treated, subtracted	Cyclohexamide Treated Cem, Jurkat, Raji, and Supt	Blood	Cell Line		pBluescript
H0222	Activated T-Cells, 8 hrs, subtracted	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0229	Early Stage Human Brain, random primed	Early Stage Human Brain	Brain			Lambda ZAP II
H0230	Human Cardiomyopathy, diff exp	Human Cardiomyopathy	Heart		disease	Uni-ZAP XR
H0231	Human Colon, subtraction	Human Colon				pBluescript
H0239	Human Kidney Tumor	Human Kidney Tumor	Kidney		disease	Uni-ZAP XR

H0242	Human Fetal Heart, Differential (Fetal-	Human Fetal Heart	Heart			pBluescript
H0244	Specific) Human 8 Week Whole Embryo, subtracted	Human 8 Week Old Embryo	Embryo			Uni-ZAP XR
H0250	Human Activated Monocytes	Human Monocytes	1			Uni-ZAP XR
H0251	Human Chondrosarcoma	Human Chondrosarcoma	Cartilage		disease	Uni-ZAP XR
H0252	Human Osteosarcoma	Human Osteosarcoma	Bone		disease	Uni-ZAP XR
H0253	Human adult testis, large inserts	Human Adult Testis	Testis			Uni-ZAP XR
H0254	Breast Lymph node cDNA library	Breast Lymph Node	Lymph Node			Uni-ZAP XR
H0255	breast lymph node CDNA library	Breast Lymph Node	Lymph Node			Lambda ZAP II
H0261	H. cerebellum, Enzyme subtracted	Human Cerebellum	Brain			Uni-ZAP XR
Н0263	human colon cancer	Human Colon Cancer	Colon		disease	Lambda ZAP II
H0264	human tonsils	Human Tonsil	Tonsil	ļ		Uni-ZAP XR
Н0265	Activated T-Cell (12hs)/Thiouridine labelledEco	T-Cells	Blood	Cell Line		Uni-ZAP XR
Н0266	Human Microvascular Endothelial Cells, fract. A	НМЕС	Vein	Cell Line		Lambda ZAP II
H0268	Human Umbilical Vein Endothelial Cells, fract. A	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0269	Human Umbilical Vein Endothelial Cells, fract. B	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0270	HPAS (human pancreas, subtracted)	Human Pancreas	Pancreas			Uni-ZAP XR
H0271	Human Neutrophil, Activated	Human Neutrophil - Activated	Blood	Cell Line		Uni-ZAP XR
H0272	HUMAN TONSILS, FRACTION 2	Human Tonsil	Tonsil			Uni-ZAP XR
H0274	Human Adult Spleen, fractionII	Human Adult Spleen	Spleen			Uni-ZAP XR
H0280	K562 + PMA (36 hrs)	K562 Cell line	cell line	Cell Line		ZAP Express Uni-ZAP XR
H0284	Human OB MG63 control fraction I	Human Osteoblastoma MG63 cell line	Bone	Cell Line		
H0286	Human OB MG63 treated (10 nM E2) fraction I	Human Osteoblastoma MG63 cell line	Bone	Cell Line		Uni-ZAP XR
H0288	Human OB HOS control fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
Н0290	Human OB HOS treated (1 nM E2) fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
Н0292	Human OB HOS treated (10 nM E2) fraction I	Human Osteoblastoma HOS cell line	Bone	Cell Line		Uni-ZAP XR
H0293	WI 38 cells			<u> </u>		Uni-ZAP XR
H0294	Amniotic Cells - TNF induced	Amniotic Cells - TNF induced	Placenta	Cell Line		Uni-ZAP XR
H0295	Amniotic Cells - Primary Culture	Amniotic Cells - Primary Culture	Placenta	Cell Line		Uni-ZAP XR
H0305	CD34 positive cells (Cord Blood)	CD34 Positive Cells	Cord Blood			ZAP Express
H0306	CD34 depleted Buffy Coat	CD34 Depleted	Cord Blood	<u> </u>		ZAP Express

	(Cord Blood)	Buffy Coat (Cord Blood)				
H0309	Human Chronic Synovitis	Synovium, Chronic Synovitis/ Osteoarthritis	Synovium		disease	Uni-ZAP XR
H0310	human caudate nucleus	Brain	Brain			Uni-ZAP XR
H0316	HUMAN STOMACH	Human Stomach	Stomach			Uni-ZAP XR
H0318	HUMAN B CELL LYMPHOMA	Human B Cell Lymphoma	Lymph Node		disease	Uni-ZAP XR
H0320	Human frontal cortex	Human Frontal Cortex	Brain			Uni-ZAP XR
H0327	human corpus colosum	Human Corpus Callosum	Brain			Uni-ZAP XR
H0328	human ovarian cancer	Ovarian Cancer	Ovary		disease	Uni-ZAP XR
H0329	Dermatofibrosarcoma Protuberance	Dermatofibrosarcom a Protuberans	Skin		disease	Uni-ZAP XR
H0331	Hepatocellular Tumor	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
H0333	Hemangiopericytoma	Hemangiopericytom a	Blood vessel		disease	Lambda ZAP II
H0334	Kidney cancer	Kidney Cancer	Kidney		disease	Uni-ZAP XR
Н0339	Duodenum	Duodenum				Uni-ZAP XR
H0340	Corpus Callosum	Corpus Collosum- 93052				Uni-ZAP XR
H0341	Bone Marrow Cell Line (RS4;11)	Bone Marrow Cell Line RS4;11	Bone Marrow	Cell Line	 	Uni-ZAP XR
H0343	stomach cancer (human)	Stomach Cancer - 5383A (human)			disease	Uni-ZAP XR
H0345	SKIN	Skin - 4000868H	Skin			Uni-ZAP XR
H0349	human adult liver cDNA library	Human Adult Liver	Liver			pCMVSport 1
H0351	Glioblastoma	Glioblastoma	Brain_		disease	Uni-ZAP XR
H0352	wilm"s tumor	Wilm"s Tumor			disease	Uni-ZAP XR
H0355	Human Liver	Human Liver, normal Adult	_			pCMVSport 1
H0359	KMH2 cell line	KMH2				ZAP Express
H0361	Human rejected kidney	Human Rejected Kidney			disease	pBluescript
H0364	Human Osteoclastoma, excised	Human Osteoclastoma			disease	pBluescript
Н0369	H. Atrophic Endometrium	Atrophic Endometrium and myometrium				Uni-ZAP XR
H0370	H. Lymph node breast Cancer	Lymph node with Met. Breast Cancer			disease	Uni-ZAP XR
H0373	Human Heart	Human Adult Heart	Heart			pCMVSport 1
H0374	Human Brain	Human Brain				pCMVSport
H0375	Human Lung	Human Lung				pCMVSport
H0379	Human Tongue, frac 1	Human Tongue				pSport1
H0386	Leukocyte and Lung; 4 screens	Human Leukocytes	Blood	Cell Line		pCMVSport 1
H0390	Human Amygdala Depression, re-excision	Human Amygdala Depression			disease	pBluescript
H0391	H. Meniingima, M6	Human Meningima	brain			pSport1
H0392	H. Meningima, M1	Human Meningima	brain			pSport1
H0393	Fetal Liver, subtraction II	Human Fetal Liver	Liver			pBluescript
H0394	A-14 cell line	Redd-Sternberg cell			ļ	ZAP Express
H0395	A1-CELL LINE	Redd-Sternberg cell	ļ			ZAP Express
Н0396	L1 Cell line	Redd-Sternberg cell	<u></u>	L	L	ZAP Express

						
H0399	Human Kidney Cortex, re-	Human Kidney]		Lambda
	rescue	Cortex		<u> </u>		ZAP II
H0402	CD34 depleted Buffy Coat (Cord Blood), re-excision	CD34 Depleted Buffy Coat (Cord Blood)	Cord Blood			ZAP Express
H0403	H. Umbilical Vein Endothelial Cells, IL4 induced	HUVE Cells	Umbilical vein	Cell Line		Uni-ZAP XR
H0404	H. Umbilical Vein endothelial cells, uninduced	HUVE Cells	Umbilical vein	Cell Line		Uni-ZAP XR
H0409	H. Striatum Depression, subtracted	Human Brain, Striatum Depression	Brain			pBluescript
H0411	H Female Bladder, Adult	Human Female Adult Bladder	Bladder			pSport1
H0412	Human umbilical vein endothelial cells, IL-4 induced	HUVE Cells	Umbilical vein	Cell Line		pSport1
H0413	Human Umbilical Vein Endothelial Cells, uninduced	HUVE Cells	Umbilical vein	Cell Line		pSport1
H0414	Ovarian Tumor I, OV5232	Ovarian Tumor, OV5232	Ovary		disease	pSport1
H0415	H. Ovarian Tumor, II, OV5232	Ovarian Tumor, OV5232	Ovary		disease	pCMVSport 2.0
H0416	Human Neutrophils, Activated, re-excision	Human Neutrophil - Activated	Blood	Cell Line		pBluescript
H0421	Human Bone Marrow, re- excision	Bone Marrow				pBluescript
H0422	T-Cell PHA 16 hrs	T-Cells	Blood	Cell Line		pSport1
H0423	T-Cell PHA 24 hrs	T-Cells	Blood	Cell Line		pSport1
H0424	Human Pituitary, subt IX	Human Pituitary				pBluescript
H0427	Human Adipose	Human Adipose, left hiplipoma				pSport1
H0428	Human Ovary	Human Ovary Tumor	Ovary			pSport1
H0429	K562 + PMA (36 hrs),re- excision	K562 Cell line	cell line	Cell Line		ZAP Express
H0431	H. Kidney Medulla, re- excision	Kidney medulla	Kidney			pBluescript
H0433	Human Umbilical Vein Endothelial cells, frac B, re-excision	HUVE Cells	Umbilical vein	Cell Line		pBluescript
H0434	Human Brain, striatum, re-excision	Human Brain, Striatum				pBluescript
H0435	Ovarian Tumor 10-3-95	Ovarian Tumor, OV350721	Ovary			pCMVSport 2.0
H0436	Resting T-Cell Library,II	T-Cells	Blood	Cell Line		pSport1
H0437	H Umbilical Vein Endothelial Cells, frac A, re-excision	HUVE Cells	Umbilical vein	Cell Line		Lambda ZAP II
H0438	H. Whole Brain #2, re- excision	Human Whole Brain #2				ZAP Express
H0441	H. Kidney Cortex, subtracted	Kidney cortex	Kidney			pBluescript
H0444	Spleen metastic melanoma	Spleen, Metastic malignant melanoma	Spleen		disease	pSport1
H0445	Spleen, Chronic lymphocytic leukemia	Human Spleen, CLL	Spleen		disease	pSport1
H0455	H. Striatum Depression, subt	Human Brain, Striatum Depression	Brain			pBluescript
H0456	H Kidney Cortex,	Human Kidney	<u> </u>	L		pBluescript

	subtracted III	Cortex	i		T	
H0457	Human Eosinophils	Human Eosinophils				pSport1
H0459	CD34+cells, II,	CD34 positive cells				pCMVSport
	FRACTION 2					2.0
H0477	Human Tonsil, Lib 3	Human Tonsil	Tonsil			pSport1
H0478	Salivary Gland, Lib 2	Human Salivary Gland	Salivary gland			pSport1
H0479	Salivary Gland, Lib 3	Human Salivary Gland	Salivary gland			pSport1
H0483	Breast Cancer cell line, MDA 36	Breast Cancer Cell line, MDA 36				pSport1
H0484	Breast Cancer Cell line, angiogenic	Breast Cancer Cell line, Angiogenic, 36T3	:			pSport1
H0485	Hodgkin"s Lymphoma I	Hodgkin"s Lymphoma I			disease	pCMVSport 2.0
H0486	Hodgkin"s Lymphoma II	Hodgkin"s Lymphoma II			disease	pCMVSport 2.0
H0487	Human Tonsils, lib I	Human Tonsils				pCMVSport
H0488	Human Tonsils, Lib 2	Human Tonsils				pCMVSport
H0489	Crohn"s Disease	Heum	Intestine		disease	pSport1
H0494	Keratinocyte	Keratinocyte				pCMVSport 2.0
H0497	HEL cell line	HEL cell line		HEL 92.1.7		pSport1
H0505	Human Astrocyte	Human Astrocyte				pSport1
H0506	Ulcerative Colitis	Colon	Colon			pSport1
H0509	Liver, Hepatoma	Human Liver, Hepatoma, patient 8	Liver		disease	pCMVSport 3.0
H0510	Human Liver, normal	Human Liver, normal, Patient # 8	Liver			pCMVSport 3.0
H0517	Nasal polyps	Nasal polyps				pCMVSport 2.0
H0518	pBMC stimulated w/ poly I/C	pBMC stimulated with poly I/C				pCMVSport 3.0
H0519	NTERA2, control	NTERA2, Teratocarcinoma cell line				pCMVSport 3.0
H0520	NTERA2 + retinoic acid, 14 days	NTERA2, Teratocarcinoma cell line				pSport1
H0521	Primary Dendritic Cells, lib 1	Primary Dendritic cells				pCMVSport 3.0
H0522	Primary Dendritic cells,frac 2	Primary Dendritic cells				pCMVSport 3.0
H0528	Poly[I]/Poly[C] Normal Lung Fibroblasts	Poly[I]/Poly[C] Normal Lung Fibroblasts				pCMVSport 3.0
H0529	Myoloid Progenitor Cell Line	TF-1 Cell Line; Myoloid progenitor cell line				pCMVSport 3.0
H0530	Human Dermal Endothelial Cells,untreated	Human Dermal Endothelial Cells; untreated				pSport1
H0538	Merkel Cells	Merkel cells	Lymph node			pSport1
H0539	Pancreas Islet Cell Tumor	Pancreas Islet Cell Tumour	Pancreas		disease	pSport1
H0540	Skin, burned	Skin, leg burned	Skin			pSport1
H0542	T Cell helper I	Helper T cell				pCMVSport
	i .	· .	{		l	3.0

H0543	T cell helper II	Helper T cell				pCMVSport 3.0
H0544	Human endometrial stromal cells	Human endometrial stromal cells				pCMVSport 3.0
H0545	Human endometrial stromal cells-treated with	Human endometrial stromal cells-treated				pCMVSport 3.0
H0546	progesterone Human endometrial stromal cells-treated with estradiol	with proge Human endometrial stromal cells-treated with estra				pCMVSport 3.0
H0547	NTERA2 teratocarcinoma cell line+retinoic acid (14 days)	NTERA2, Teratocarcinoma cell line				pSport1
Н0549	H. Epididiymus, caput & corpus	Human Epididiymus, caput and corpus				Uni-ZAP XR
H0550	H. Epididiymus, cauda	Human Epididiymus, cauda				Uni-ZAP XR
H0551	Human Thymus Stromal Cells	Human Thymus Stromal Cells				pCMVSport 3.0
H0553	Human Placenta	Human Placenta				pCMVSport 3.0
H0555	Rejected Kidney, lib 4	Human Rejected Kidney	Kidney		disease	pCMVSport 3.0
Н0556	Activated T- cell(12h)/Thiouridine-re- excision	T-Cells	Blood	Cell Line		Uni-ZAP XR
H0559	HL-60, PMA 4H, re- excision	HL-60 Cells, PMA stimulated 4H	Blood	Cell Line		Uni-ZAP XR
H0560	КМН2	КМН2				pCMVSport 3.0
H0561	L428	L428				pCMVSport 3.0
H0562	Human Fetal Brain, normalized c5-11-26	Human Fetal Brain				pCMVSport 2.0
H0563	Human Fetal Brain, normalized 50021F	Human Fetal Brain				pCMVSport 2.0
H0564	Human Fetal Brain, normalized C5001F	Human Fetal Brain				pCMVSport 2.0
H0566	Human Fetal Brain,normalized c50F	Human Fetal Brain				pCMVSport 2.0
H0569	Human Fetal Brain, normalized CO	Human Fetal Brain				pCMVSport 2.0
H0570	Human Fetal Brain, normalized C500H	Human Fetal Brain				pCMVSport 2.0
H0571	Human Fetal Brain, normalized C500HE	Human Fetal Brain				pCMVSport 2.0
H0572	Human Fetal Brain, normalized AC5002	Human Fetal Brain				pCMVSport 2.0
H0574	Hepatocellular Tumor; re- excision	Hepatocellular Tumor	Liver		disease	Lambda ZAP II
H0575	Human Adult Pulmonary;re-excision	Human Adult Pulmonary	Lung			Uni-ZAP XR
H0576	Resting T-Cell; re-	T-Cells	Blood	Cell Line		Lambda ZAP II
H0579	Pericardium	Pericardium	Heart			pSport1
H0580	Dendritic cells, pooled	Pooled dendritic cells				pCMVSport 3.0
H0581	Human Bone Marrow, treated	Human Bone Marrow	Bone Marrow			pCMVSport 3.0
H0583	B Cell lymphoma	B Cell Lymphoma	B Cell		disease	pCMVSport 3.0
H0586	Healing groin wound, 6.5	healing groin	groin		disease	pCMVSport

[hours post incision	wound, 6.5 hours	:		3.0
		post incision - 2/			<u> </u>
H0587	Healing groin wound; 7.5 hours post incision	Groin-2/19/97	groin	disease	pCMVSport 3.0
H0589	CD34 positive cells (cord blood),re-ex	CD34 Positive Cells	Cord Blood		ZAP Express
H0590	Human adult small intestine, re-excision	Human Adult Small Intestine	Small Int.		Uni-ZAP XR
H0591	Human T-cell lymphoma;re-excision	T-Cell Lymphoma	T-Cell	disease	Uni-ZAP XR
H0592	Healing groin wound - zero hr post-incision (control)	HGS wound healing project; abdomen		disease	pCMVSport 3.0
H0593	Olfactory epithelium;nasalcavity	Olfactory epithelium from roof of left nasal cacit			pCMVSport 3.0
H0594	Human Lung Cancer;re- excision	Human Lung Cancer	Lung	disease	Lambda ZAP II
H0595	Stomach cancer (human);re-excision	Stomach Cancer - 5383A (human)		disease	Uni-ZAP XR
H0596	Human Colon Cancer;re- excision	Human Colon Cancer	Colon		Lambda ZAP II
H0597	Human Colon; re-excision	Human Colon			Lambda ZAP II
H0598	Human Stomach;re- excision	Human Stomach	Stomach		Uni-ZAP XR
H0599	Human Adult Heart;re- excision	Human Adult Heart	Heart		Uni-ZAP XR
H0600	Healing Abdomen wound;70&90 min post incision	Abdomen		disease	pCMVSport 3.0
H0601	Healing Abdomen Wound;15 days post incision	Abdomen		disease	pCMVSport 3.0
H0604	Human Pituitary, re- excision	Human Pituitary			pBluescript
H0606	Human Primary Breast Cancer; re-excision	Human Primary Breast Cancer	Breast	disease	Uni-ZAP XR
H0608	H. Leukocytes, control	H.Leukocytes			pCMVSport
H0609	H. Leukocytes, normalized cot > 500A	H.Leukocytes			pCMVSport
H0614	H. Leukocytes, normalized cot 500 A	H.Leukocytes			pCMVSport
H0615	Human Ovarian Cancer Reexcision	Ovarian Cancer	Ovary	disease	Uni-ZAP XR
H0616	Human Testes, Reexcision	Human Testes	Testis		Uni-ZAP XR
H0617	Human Primary Breast Cancer Reexcision	Human Primary Breast Cancer	Breast	disease	Uni-ZAP XR
H0618	Human Adult Testes, Large Inserts, Reexcision	Human Adult Testis	Testis		Uni-ZAP XR
H0619	Fetal Heart	Human Fetal Heart	Heart		Uni-ZAP XR
H0620	Human Fetal Kidney; Reexcision	Human Fetal Kidney	Kidney		Uni-ZAP XR
H0622	Human Pancreas Tumor; Reexcision	Human Pancreas Tumor	Pancreas	disease	Uni-ZAP XR
H0623	Human Umbilical Vein; Reexcision	Human Umbilical Vein Endothelial Cells	Umbilical vein		Uni-ZAP XR
H0624	12 Week Early Stage Human II; Reexcision	Twelve Week Old Early Stage Human	Embryo		Uni-ZAP XR
H0625	Ku 812F Basophils Line	Ku 812F Basophils			pSport1
H0626	Saos2 Cells; Untreated	Saos2 Cell Line;			pSport1

		Untreated				
H0628	Human Pre-Differentiated	Human Pre-		i i		Uni-ZAP XR
	Adipocytes	Differentiated				
H0631	Saos2, Dexamethosome	Adipocytes Saos2 Cell Line;		 		pSport1
поозт	Treated	Dexamethosome		{		ророн
	Treates	Treated		(1
H0632	Hepatocellular Tumor;re-	Hepatocellular	Liver			Lambda
	excision	Tumor				ZAPII
H0633	Lung Carcinoma A549 TNFalpha activated	TNFalpha activated A549Lung		1	disease	pSport1
	INFaipha activated	Carcinoma		({
H0634	Human Testes Tumor, re-	Human Testes	Testis		disease	Uni-ZAP XR
	excision	Tumor		[]		
H0635	Human Activated T-Cells, re-excision	Activated T-Cells	Blood	Cell Line		Uni-ZAP XR
H0637	Dendritic Cells From	Dentritic cells from				pSport1
	CD34 Cells	CD34 cells				
H0638	CD40 activated monocyte	CD40 activated				pSport1
	dendridic cells	monocyte dendridic cells]]
H0639	Ficolled Human Stromal	Ficolled Human		 		Other
110037	Cells, 5Fu treated	Stromal Cells, 5Fu		, ,		1
		treated				<u> </u>
H0641	LPS activated derived	LPS activated				pSport1
	dendritic cells	monocyte derived		1		,
110642	Han C2 Calle Jambda	dendritic cells Hep G2 Cells		}		Other
H0642	Hep G2 Cells, lambda library	nep 02 Cells) j		Other
H0643	Hep G2 Cells, PCR library	Hep G2 Cells				Other
H0644	Human Placenta (re-	Human Placenta	Placenta			Uni-ZAP XR
	excision)					<u> </u>
H0645	Fetal Heart, re-excision	Human Fetal Heart	Heart	ļ	· 	Uni-ZAP XR
H0646	Lung, Cancer (4005313 A3): Invasive Poorly	Metastatic squamous cell lung		ļ		pSport1
	Differentiated Lung	carcinoma, poorly di				}
	Adenocarcinoma,					<u> </u>
H0647	Lung, Cancer (4005163	Invasive poorly			disease	pSport1
	B7): Invasive, Poorly Diff.	differentiated lung			i	
	Adenocarcinoma,	adenocarcinoma				j
H0648	Metastatic Ovary, Cancer: (4004562	Papillary Cstic		 	disease	pSport1
110040	B6) Papillary Serous	neoplasm of low	i			F-F
	Cystic Neoplasm, Low	malignant potentia	i			
	Malignant Pot			<u> </u>		
H0649	Lung, Normal: (4005313	Normal Lung	i			pSport1
H0650	B1) B-Cells	B-Cells		 		pCMVSport
110050) D dens	5 000				3.0
H0651	Ovary, Normal: (9805C040R)	Normal Ovary				pSport1
H0652	Lung, Normal: (4005313	Normal Lung				pSport1
H0653	Stromal Cells	Stromal Cells		<u> </u>		pSport1
H0656	B-cells (unstimulated)	B-cells				pSport1
		(unstimulated)		<u> </u>		
H0657	B-cells (stimulated)	B-cells (stimulated)			1:	pSport1
H0658	Ovary, Cancer	9809C332- Poorly differentiate	Ovary & Fallopian		disease	pSport1
	(9809C332): Poorly differentiated	differentiale	Tubes			j
	adenocarcinoma		. 2000			
H0659	Ovary, Cancer	Grade II Papillary	Ovary		disease	pSport1
	(15395A1F): Grade II	Carcinoma, Ovary		L		

	Papillary Carcinoma				
H0660	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	Poorly differentiated carcinoma, ovary		disease	pSport1
H0661	Breast, Cancer: (4004943 A5)	Breast cancer		disease	pSport1
H0662	Breast, Normal: (4005522B2)	Normal Breast - #4005522(B2)	Breast		pSport1
H0663	Breast, Cancer: (4005522 A2)	Breast Cancer - #4005522(A2)	Breast	disease	pSport1
H0664	Breast, Cancer: (9806C012R)	Breast Cancer	Breast	disease	pSport1
H0665	Stromal cells 3.88	Stromal cells 3.88			pSport1
Н0666	Ovary, Cancer: (4004332 A2)	Ovarian Cancer, Sample #4004332A2		disease	pSport1
H0667	Stromal cells(HBM3.18)	Stromal cell(HBM 3.18)			pSporti
H0668	stromal cell clone 2.5	stromal cell clone 2.5			pSport1
Н0670	Ovary, Cancer(4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma	Ovarian Cancer - 4004650A3			pSport1
H0672	Ovary, Cancer: (4004576 A8)	Ovarian Cancer(4004576A8)	Ovary		pSport1
Н0673	Human Prostate Cancer, Stage B2; re-excision	Human Prostate Cancer, stage B2	Prostate		Uni-ZAP XR
H0674	Human Prostate Cancer, Stage C; re-excission	Human Prostate Cancer, stage C	Prostate		Uni-ZAP XR
H0675	Colon, Cancer: (9808C064R)	Colon Cancer 9808C064R			pCMVSport 3.0
H0676	Colon, Cancer: (9808C064R)-total RNA	Colon Cancer 9808C064R			pCMVSport 3.0
H0677	TNFR degenerate oligo	B-Cells			PCRII
Н0682	Serous Papillary Adenocarcinoma	serous papillary adenocarcinoma (9606G304SPA3B)			pCMVSport 3.0
H0683	Ovarian Serous Papillary Adenocarcinoma	Serous papillary adenocarcinoma, stage 3C (9804G01			pCMVSport 3.0
H0684	Serous Papillary Adenocarcinoma	Ovarian Cancer- 9810G606	Ovaries		pCMVSport 3.0
H0685	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-3	Adenocarcinoma of Ovary, Human Cell Line, # OVCAR-			pCMVSport 3.0
H0686	Adenocarcinoma of Ovary, Human Cell Line	Adenocarcinoma of Ovary, Human Cell Line, # SW-626			pCMVSport 3.0
H0687	Human normal ovary(#9610G215)	Human normal ovary(#9610G215)	Ovary		pCMVSport 3.0
H0688	Human Ovarian Cancer(#9807G017)	Human Ovarian cancer(#9807G017), mRNA from Maura Ru			pCMVSport 3.0
H0689	Ovarian Cancer	Ovarian Cancer, #9806G019			pCMVSport 3.0
H0690	Ovarian Cancer, # 9702G001	Ovarian Cancer, #9702G001			pCMVSport 3.0
H0692	BLyS Receptor from Expression Cloning	B Cell Lymphoma	B Cell		pCMVSport 3.0
H0693	Normal Prostate #ODQ3958EN	Normal Prostate Tissue #			pCMVSport 3.0

		ODQ3958EN				GN 41 / G
H0695	mononucleocytes from	mononucleocytes				pCMVSport
	patient	from patient at				3.0
		Shady Grove Hospit				
N0006	Human Fetal Brain	Human Fetal Brain				Lambda
S0001	Brain frontal cortex	Brain frontal cortex	Brain	ì		ZAP II
		3.6	blood	Cell Line		Uni-ZAP XR
S0002	Monocyte activated	Monocyte-activated	blood	Cell Line	disease	Uni-ZAP XR
S0003	Human Osteoclastoma	Osteoclastoma	bone Heart 0		disease	pCDNA
S0005	Heart	Heart-left ventricle	Heart 0			Uni-ZAP XR
S0007_	Early Stage Human Brain	Human Fetal Brain				Uni-ZAP XR
S0010	Human Amygdala	Amygdala	t		disease	Uni-ZAP XR
S0011	STROMAL - OSTEOCLASTOMA	Osteoclastoma	bone		disease	
S0013	Prostate	Prostate	prostate			Uni-ZAP XR
S0014	Kidney Cortex	Kidney cortex	Kidney			Uni-ZAP XR
S0022	Human Osteoclastoma Stromal Cells - unamplified	Osteoclastoma Stromal Cells				Uni-ZAP XR
S0023	Human Kidney Cortex - unamplified	Human Kidney Cortex				
S0024	Human Kidney Medulla - unamplified	Human Kidney Medulla				
S0026	Stromal cell TF274	stromal cell	Bone marrow	Cell Line		Uni-ZAP XR
S0020 S0027	Smooth muscle, serum treated	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0028	Smooth muscle,control	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0029	brain stem	Brain stem	brain			Uni-ZAP XR
S0029 S0030	Brain pons	Brain Pons	Brain			Uni-ZAP XR
S0030	Spinal cord	Spinal cord	spinal cord			Uni-ZAP XR
S0031	Smooth muscle-ILb induced	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XR
S0036	Human Substantia Nigra	Human Substantia Nigra				Uni-ZAP XR
S0037	Smooth muscle, IL1b	Smooth muscle	Pulmanary artery	Cell Line		Uni-ZAP XF
S0038	Human Whole Brain #2 - Oligo dT > 1.5Kb	Human Whole Brain #2				ZAP Express
S0040	Adipocytes	Human Adipocytes from Osteoclastoma				Uni-ZAP XI
S0042	Testes	Human Testes				ZAP Expres
S0044	Prostate BPH	prostate BPH	Prostate		disease	Uni-ZAP XI
S0045	Endothelial cells-control	Endothelial cell	endothelial cell-lung	Cell Line		Uni-ZAP XI
S0046	Endothelial-induced	Endothelial cell	endothelial cell-lung	Cell Line		Uni-ZAP XI
S0049	Human Brain, Striatum	Human Brain, Striatum				Uni-ZAP XI
S0050	Human Frontal Cortex, Schizophrenia	Human Frontal Cortex, Schizophrenia			disease	Uni-ZAP X
S0051	Human Hypothalmus,Schizophren	Human Hypothalamus, Schizophrenia			disease	Uni-ZAP X
00050	ia	human neutrophils	blood	Cell Line		Uni-ZAP X
S0052 S0053	neutrophils control Neutrophils IL-1 and LPS	human neutrophil	blood .	Cell Line		Uni-ZAP X
S0106	STRIATUM	induced	BRAIN		disease	Uni-ZAP X
	DEPRESSION		Brain	 		Uni-ZAP X
S0112 S0114	Hypothalamus Anergic T-cell	Anergic T-cell	Dialit	Cell Line	 	Uni-ZAP X

S0116	Bone marrow	Bone marrow	Bone marrow			Uni-ZAP XR
S0122	Osteoclastoma-normalized A	Osteoclastoma	bone		disease	pBluescript
S0126	Osteoblasts	Osteoblasts	Knee	Cell Line		Uni-ZAP XR
S0132	Epithelial-TNFa and INF induced	Airway Epithelial				Uni-ZAP XR
S0134	Apoptotic T-cell	apoptotic cells		Cell Line		Uni-ZAP XR
S0136	PERM TF274	stromal cell	Bone marrow	Cell Line		Lambda ZAP II
S0142	Macrophage-oxLDL	macrophage- oxidized LDL treated	blood	Cell Line		Uni-ZAP XR
S0144	Macrophage (GM-CSF treated)	Macrophage (GM- CSF treated)				Uni-ZAP XR
S0146	prostate-edited	prostate BPH	Prostate			Uni-ZAP XR
S0148	Normal Prostate	Prostate	prostate			Uni-ZAP XR
S0150	LNCAP prostate cell line	LNCAP Cell Line	Prostate	Cell Line		Uni-ZAP XR
S0152	PC3 Prostate cell line	PC3 prostate cell line				Uni-ZAP XR
S0168	Prostate/LNCAP, subtraction I	PC3 prostate cell line				pBluescript
S0174	Prostate-BPH subtracted II	Human Prostate BPH				pBluescript
S0182	Human B Cell 8866	Human B- Cell 8866				Uni-ZAP XR
S0192	Synovial Fibroblasts (control)	Synovial Fibroblasts				pSport1
S0194	Synovial hypoxia	Synovial Fibroblasts				pSport1
S0196	Synovial IL-1/TNF stimulated	Synovial Fibroblasts				pSport1
S0198	7TM-pbfd	PBLS, 7TM receptor enriched			•	PCRII
S0206	Smooth Muscle- HASTE normalized	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S0208	Messangial cell, frac 1	Messangial cell	-			pSport1
S0210	Messangial cell, frac 2	Messangial cell				pSport1
S0212	Bone Marrow Stromal Cell, untreated	Bone Marrow Stromal Cell,untreated				pSport1
S0214	Human Osteoclastoma, re- excision	Osteoclastoma	bone		disease	Uni-ZAP XR
S0216	Neutrophils IL-1 and LPS induced	human neutrophil induced	blood	Cell Line		Uni-ZAP XR
S0218	Apoptotic T-cell, re-	apoptotic cells		Cell Line		Uni-ZAP XR
S0220	H. hypothalamus, frac A;re-excision	Hypothalamus	Brain			ZAP Express
S0222	H. Frontal cortex,epileptic;re- excision	H. Brain, Frontal Cortex, Epileptic	Brain		disease	Uni-ZAP XR
S0228	PSMIX	PBLS, 7TM receptor enriched				PCRII
S0242	Synovial Fibroblasts (II1/TNF), subt	Synovial Fibroblasts				pSport1
S0250	Human Osteoblasts II	Human Osteoblasts	Femur		disease	pCMVSport 2.0
S0252	7TM-PIMIX	PBLS, 7TM receptor enriched				PCRII
S0260	Spinal Cord, re-excision	Spinal cord	spinal cord			Uni-ZAP XR
S0264	PPMIX	PPMIX (Human Pituitary)	Pituitary			PCRII
S0268	PRMIX	PRMIX (Human Prostate)	prostate			PCRII

S0270	PTMIX	PTMIX (Human	Thymus		<u></u>	PCRII
S0274	PCMIX	Thymus) PCMIX (Human	Brain			PCRII
S0276	Synovial hypoxia-RSF	Cerebellum) Synovial fobroblasts	Synovial			pSport1
S0278	subtracted H Macrophage (GM-CSF	(rheumatoid) Macrophage (GM-	tissue		<u></u>	Uni-ZAP XR
S0280	treated), re-excision Human Adipose Tissue,	CSF treated) Human Adipose				Uni-ZAP XR
S0282	re-excision Brain Frontal Cortex, re-	Tissue Brain frontal cortex	Brain			Lambda ZAP II
S0294	excision Larynx tumor	Larynx tumor	Larynx,vocal cord		disease	pSport1
S0298	Bone marrow stroma,treated	Bone marrow stroma,treatedSB	Bone marrow			pSport1
S0300	Frontal lobe,dementia;re- excision	Frontal Lobe dementia/Alzheimer'	Brain			Uni-ZAP XR
S0306	Larynx normal #10 261- 273	Larynx normal				pSport1
S0308	Spleen/normal	Spleen normal				pSport1
S0310	Normal trachea	Normal trachea				pSport1
S0312	Human osteoarthritic;fraction II	Human osteoarthritic cartilage			disease	pSport1
S0314	Human osteoarthritis; fraction I	Human osteoarthritic cartilage			disease	pSport1
S0316	Human Normal Cartilage,Fraction I	Human Normal Cartilage				pSport1
S0318	Human Normal Cartilage Fraction II	Human Normal Cartilage				pSport1
S0328	Palate carcinoma	Palate carcinoma	Uvula		disease	pSport1
S0330	Palate normal	Palate normal	Uvula			pSport1
S0332	Pharynx carcinoma	Pharynx carcinoma	Hypopharynx			pSport1
S0334	Human Normal Cartilage Fraction III	Human Normal Cartilage				pSport1
S0338	Human Osteoarthritic Cartilage Fraction III	Human osteoarthritic cartilage			disease	pSport1
S0340	Human Osteoarthritic Cartilage Fraction IV	Human osteoarthritic cartilage			disease	pSport1
S0342	Adipocytes;re-excision	Human Adipocytes from Osteoclastoma				Uni-ZAP XR
S0344	Macrophage-oxLDL; re- excision	macrophage- oxidized LDL treated	blood	Cell Line		Uni-ZAP XR
S0346	Human Amygdala;re- excision	Amygdala				Uni-ZAP XR
S0350	Pharynx Carcinoma	Pharynx carcinoma	Hypopharynx		disease	pSport1
S0352	Larynx Carcinoma	Larynx carcinoma			disease	pSport1
S0354	Colon Normal II	Colon Normal	Colon			pSport1
S0356	Colon Carcinoma	Colon Carcinoma	Colon		disease	pSport1
S0358	Colon Normal III	Colon Normal	Colon			pSport1
S0360	Colon Tumor II	Colon Tumor	Colon		disease	pSport1
S0362	Human Gastrocnemius	Gastrocnemius muscle				pSport1
S0364	Human Quadriceps	Quadriceps muscle				pSport1
S0366	Human Soleus	Soleus Muscle				pSport1
• •	Larynx carcinoma II	Larynx carcinoma		1	disease	pSport1

S0374	Normal colon	Normal colon		 		pSport1
S0374	Colon Tumor	Colon Tumor		 	discase	pSport1
S0378	Pancreas normal PCA4	Pancreas Normal PCA4 No			discuss	pSport1
S0380	Pancreas Tumor PCA4 Tu	Pancreas Tumor PCA4 Tu			disease	pSport1
S0386	Human Whole Brain, re-	Whole brain	Brain			ZAP Express
S0388	excision Human Hypothalamus,schizophre	Human Hypothalamus,			disease	Uni-ZAP XR
S0390	nia, re-excision Smooth muscle, control;	Schizophrenia Smooth muscle	Pulmanary	Cell Line		Uni-ZAP XR
S0392	re-excision Salivary Gland	Salivary gland;	artery			pSport1
		normal				
S0400	Brain; normal	Brain; normal		l		pSport1
S0404	Rectum normal	Rectum, normal				pSport1
\$0406	Rectum tumour	Rectum tumour				pSport1
S0408	Colon, normal	Colon, normal			<u>-</u>	pSport1
S0410	Colon, tumour	Colon, tumour				pSport1
S0412	Temporal cortex- Alzheizmer; subtracted	Temporal cortex, alzheimer			disease	Other
S0414	Hippocampus, Alzheimer Subtracted	Hippocampus, Alzheimer Subtracted				Other
S0418	CHME Cell Line;treated 5 hrs	CHME Cell Line; treated				pCMVSport 3.0
S0420	CHME Cell Line,untreated	CHME Cell line, untreatetd				pSport1
S0422	Mo7e Cell Line GM-CSF treated (lng/ml)	Mo7e Cell Line GM-CSF treated (1ng/ml)				pCMVSport 3.0
S0424	TF-1 Cell Line GM-CSF Treated	TF-1 Cell Line GM-CSF Treated				pSport1
S0426	Monocyte activated; re- excision	Monocyte-activated	blood	Cell Line		Uni-ZAP XR
S0428	Neutrophils control; re- excision	human neutrophils	blood	Cell Line		Uni-ZAP XR
S0430	Aryepiglottis Normal	Aryepiglottis Normal				pSport1
S0432	Sinus piniformis Tumour	Sinus piniformis Tumour				pSport1
S0434	Stomach Normal	Stomach Normal			disease	pSport1
S0436	Stomach Tumour	Stomach Tumour			disease	pSport1
S0438	Liver Normal Met5No	Liver Normal Met5No				pSport1
S0440	Liver Tumour Met 5 Tu	Liver Tumour				pSport1
S0442	Colon Normal	Colon Normal				pSport1
S0444	Colon Tumor	Colon Tumour			disease	pSport1
S0446	Tongue Tumour	Tongue Tumour				pSport1
S0448	Larynx Normal	Larynx Normal				pSport1
S0450	Larynx Tumour	Larynx Tumour				pSport1
S0452	Thymus	Thymus				pSport1
S0456	Tongue Normal	Tongue Normal				pSport1
S0458	Thyroid Normal (SDCA2 No)	Thyroid normal				pSport1
S0460	Thyroid Tumour	Thyroid Tumour			· · · · · · · · · · · · · · · · · · ·	pSport1
S0462	Thyroid Thyroiditis	Thyroid Thyroiditis		1		pSport1
S0464	Larynx Normal	Larynx Normal		 		pSport1
			<u> </u>	+		pSport1
	Ea by 926 cell line	l Ea.hv.926 cell line				
S0468 S0472	Ea.hy.926 cell line Lung Mesothelium	Ea.hy.926 cell line PYBT		 		pSport1

		T	platelets	1		
S0665	Human Amygdala; re- excission	Amygdala				Uni-ZAP XR
S3012	Smooth Muscle Serum Treated, Norm	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S3014	Smooth muscle, serum induced,re-exc	Smooth muscle	Pulmanary artery	Cell Line		pBluescript
S6014	H. hypothalamus, frac A	Hypothalamus	Brain			ZAP Express
S6016	H. Frontal Cortex, Epileptic	H. Brain, Frontal Cortex, Epileptic	Brain		disease	Uni-ZAP XR
S6022	H. Adipose Tissue	Human Adipose Tissue				Uni-ZAP XR
S6024	Alzheimers, spongy change	Alzheimer"s/Spongy change	Brain		disease	Uni-ZAP XR
S6026	Frontal Lobe, Dementia	Frontal Lobe dementia/Alzheimer' 's	Brain			Uni-ZAP XR
S6028	Human Manic Depression Tissue	Human Manic depression tissue	Brain		disease	Uni-ZAP XR
T0002	Activated T-cells	Activated T-Cell, PBL fraction	Blood	Cell Line		pBluescript SK-
T0003	Human Fetal Lung	Human Fetal Lung				pBluescript SK-
T0004	Human White Fat	Human White Fat				pBluescript SK-
T0006	Human Pineal Gland	Human Pinneal Gland				pBluescript SK-
T0008	Colorectal Tumor	Colorectal Tumor			disease	pBluescript SK-
T0010	Human Infant Brain	Human Infant Brain				Other
T0023	Human Pancreatic Carcinoma	Human Pancreatic Carcinoma			disease	pBluescript SK-
T0039	HSA 172 Cells	Human HSA172 cell line				pBluescript SK-
T0040	HSC172 cells	SA172 Cells				pBluescript SK-
T0041	Jurkat T-cell G1 phase	Jurkat T-cell				pBluescript SK-
T0042	Jurkat T-Cell, S phase	Jurkat T-Cell Line			·	pBluescript SK-
T0048	Human Aortic Endothelium	Human Aortic Endothilium			··	pBluescript SK-
T0049	Aorta endothelial cells + TNF-a	Aorta endothelial cells				pBluescript SK-
T0060	Human White Adipose	Human White Fat				pBluescript SK-
T0067	Human Thyroid	Human Thyroid				pBluescript SK-
T0068	Normal Ovary, Premenopausal	Normal Ovary, Premenopausal				pBluescript SK-
T0069	Human Uterus, normal	Human Uterus, normal	. <u> </u>			pBluescript SK-
T0071	Human Bone Marrow	Human Bone Marrow				pBluescript SK-
T0082	Human Adult Retina	Human Adult Retina				pBluescript SK-
T0109	Human (HCC) cell line liver (mouse) metastasis, remake					pBluescript SK-
T0110	Human colon carcinoma (HCC) cell line, remake					pBluescript SK-
T0114	Human (Caco-2) cell line,	<u> </u>		<u> </u>		pBluescript

	adenocarcinoma, colon,	<u></u>			SK-
50115	remake				pBluescript
T0115	Human Colon Carcinoma (HCC) cell line				SK-
L0002	Atrium cDNA library Human heart				
L0004	ClonTech HL 1065a				
L0005	Clontech human aorta polyA+ mRNA (#6572)				
L0015	Human				
L0021	Human adult (K.Okubo)				
L0022	Human adult lung 3"				
	directed Mbol cDNA				
L0040	Human colon mucosa				
L0053	Human pancreatic tumor				
L0055	Human promyelocyte				
L0096	Subtracted human retina				
L0097	Subtracted human retinal pigment epithelium (RPE)				·
L0103	DKFZphamyl	amygdala			
L0105	Human aorta polyA+ (TFujiwara)	aorta			
L0109	Human brain cDNA	brain			
L0118	Human fetal brain S. Meier-Ewert	brain			
L0142	Human placenta cDNA (TFujiwara)	placenta			
L0143	Human placenta polyA+ (TFujiwara)	placenta			
L0151	Human testis (C. De Smet)	testis			
L0157	Human fetal brain (TFujiwara)		brain		
L0163	Human heart cDNA (YNakamura)		heart		
L0351	Infant brain, Bento Soares				BA, M13-
					derived
L0352	Normalized infant brain, Bento Soares				BA, M13- derived
L0356	S, Human foetal Adrenals tissue				Bluescript
L0361	Stratagene ovary (#937217)		ovary		Bluescript SK
L0362	Stratagene ovarian cancer (#937219)				Bluescript SK-
L0363	NCI_CGAP_GC2	germ cell tumor			Bluescript SK-
L0364	NCI_CGAP_GC5	germ cell tumor			Bluescript SK-
L0365	NCI_CGAP_Phe1	pheochromocytoma			Bluescript SK-
L0366	Stratagene schizo brain	schizophrenic brain S-11 frontal lobe			Bluescript SK-
L0367	NCI_CGAP_Sch1	Schwannoma tumor			Bluescript SK-
L0368	NCI_CGAP_SS1	synovial sarcoma			Bluescript SK-
L0369	NCI_CGAP_AA1	adrenal adenoma	adrenal gland		Bluescript SK-
L0370	Johnston frontal cortex	pooled frontal lobe	brain		Bluescript SK-
	P .	L	breast	 - 	Bluescript

			· · · · · · · · · · · · · · · · · · ·		SK-
L0372	NCI_CGAP_Co12	colon tumor	colon		Bluescript SK-
L0373	NCI_CGAP_Col1	tumor	colon		Bluescript SK-
L0374	NCI_CGAP_Co2	tumor	colon		Bluescript SK-
L0375	NCI_CGAP_Kid6	kidney tumor	kidney		Bluescript SK-
L0376	NCI_CGAP_Lar1	larynx	larynx		Bluescript SK-
L0378	NCI_CGAP_Lu1	lung tumor	lung		Bluescript SK-
L0381	NCI_CGAP_HN4	squamous cell carcinoma	pharynx		Bluescript SK-
L0383	NCI_CGAP_Pr24	invasive tumor (cell line)	prostate		Bluescript SK-
L0384	NCI_CGAP_Pr23	prostate tumor	prostate		Bluescript SK-
L0386	NCI_CGAP_HN3	squamous cell carcinoma from base of tongue	tongue		Bluescript SK-
L0387	NCI_CGAP_GCB0	germinal center B- cells	tonsil		Bluescript SK-
L0388	NCI_CGAP_HN6	normal gingiva (cell line from immortalized kerati			Bluescript SK-
L0389	NCI_CGAP_HN5	normal gingiva (cell line from primary keratinocyt			Bluescript SK-
L0394	H, Human adult Brain Cortex tissue				gt11
L0415	b4HB3MA Cot8-HAP-Ft				Lafmid BA
L0418	b4HB3MA-Cot109+10- Bio				Lafmid BA
L0435	Infant brain, LLNL array of Dr. M. Soares 1NIB				lafmid BA
L0438	normalized infant brain cDNA	total brain	brain		lafmid BA
L0439	Soares infant brain 1NIB		whole brain		Lafmid BA
L0455	Human retina cDNA randomly primed sublibrary	retina	eye		lambda gt10
L0456	Human retina cDNA Tsp5091-cleaved sublibrary	retina	eye		lambda gt10
L0462	WATM1				lambda gt l 1
L0465	TEST1, Human adult Testis tissue				lambda nm1149
L0471	Human fetal heart, Lambda ZAP Express				Lambda ZAP Express
L0475	KG1-a Lambda Zap Express cDNA library			KG1-a	Lambda Zap Express (Stratagene)
L0483	Human pancreatic islet				Lambda ZAPII
L0485	STRATAGENE Human skeletal muscle cDNA library, cat. #936215.	skeletal muscle	leg muscle		Lambda ZAPII
L0502	NCI CGAP Br15	adenocarcinoma	breast		pAMP1
L0514	NCI_CGAP_Ov31	papillary serous carcinoma	ovary		pAMP1
L0517	NCI_CGAP_PrI				pAMP10

				,		·
L0518	NCI_CGAP_Pr2					pAMP10
L0519	NCI_CGAP_Pr3					pAMP10
L0520	NCI_CGAP_AIvI	alveolar				pAMP10
		rhabdomyosarcoma				
L0521	NCI_CGAP_Ew1	Ewing"s sarcoma				pAMP10
L0523	NCI_CGAP_Lip2	liposarcoma				pAMP10
L0526	NCI_CGAP_Pr12	metastatic prostate				pAMP10
		bone lesion				
L0527	NCI_CGAP_Ov2	ovary	ļ <u>.</u>			pAMP10
L0528	NCI_CGAP_Pr5	prostate				pAMP10
L0529	NCI_CGAP_Pr6	prostate			· 	pAMP10
L0530	NCI_CGAP_Pr8	prostate	ļ		<u></u>	pAMP10
L0533	NCI_CGAP_HSC1	stem cells	bone marrow			pAMP10
L0534	Chromosome 7 Fetal Brain cDNA Library	brain	brain		<u> </u>	pAMP10
L0540	NCI_CGAP_Pr10	invasive prostate tumor	prostate			pAMP10
L0542	NCI_CGAP_Prl1	normal prostatic epithelial cells	prostate			pAMP10
L0545	NCJ_CGAP_Pr4.1	prostatic intraepithelial ncoplasia - high grade	prostate			pAMP10
L0546	NCI CGAP Pr18	stroma	prostate			pAMP10
L0547	NCI CGAP Pr16	tumor	prostate			pAMP10
L0549	NCI_CGAP_HN10	carcinoma in situ from retromolar trigone				pAMP10
L0551	NCI_CGAP_HN7	normal squamous epithelium, floor of mouth				pAMP10
L0558	NCI_CGAP_Ov40	endometrioid ovarian metastasis	ovary			pAMP10
L0562	Chromosome 7 HeLa cDNA Library			HeLa cell line; ATCC		pAMP10
L0563	Human Bone Marrow Stromal Fibroblast	bone marrow				pBluescript
L0564	Jia bone marrow stroma	bone marrow stroma				pBluescript
L0565	Normal Human Trabecular Bone Cells	Bone	Hip			pBluescript
L0581	Stratagene liver (#937224)		liver			pBluescript SK
L0584	Stratagene cDNA library Human heart, cat#936208					pBluescript SK(+)
L0588	Stratagene endothelial cell 937223					pBluescript SK-
L0589	Stratagene fetal retina 937202					pBluescript SK-
L0590	Stratagene fibroblast (#937212)					pBluescript SK-
L0591	Stratagene HeLa cell s3 937216					pBluescript SK-
L0592	Stratagene hNT neuron (#937233)					pBluescript SK-
L0593	Stratagene neuroepithelium (#937231)					pBluescript SK-
L0594	Stratagene neuroepithelium NT2RAMI 937234					pBluescript SK-
L0595	Stratagene NT2 neuronal	neuroepithelial cells	brain]	pBluescript

	777777777777777777777777777777777777777					SK-
L0596	precursor 937230 Stratagene colon		colon			pBluescript
L0390	(#937204)		••••			SK-
L0597	Stratagene corneal stroma		cornea			pBluescript
20007	(#937222)					SK-
L0598	Morton Fetal Cochlea	cochlea	ear	,		pBluescript
						SK-
L0599	Stratagene lung (#937210)		lung			pBluescript
						SK-
L0600	Weizmann Olfactory	olfactory epithelium	nose			pBluescript SK-
	Epithelium			<u> </u>		pBluescript
L0601	Stratagene pancreas	· 1	pancreas			SK-
	(#937208)	pancreatic islet	nanarons			pBluescript
L0602	Pancreatic Islet	pancreatic islet	pancreas			SK-
1.0603	Sttlocanto		placenta			pBluescript
L0603	Stratagene placenta (#937225)		pracerna			SK-
L0604	Stratagene muscle 937209	muscle	skeletal			pBluescript
L0004	Stratagene musere 757207		muscle			SK-
L0605	Stratagene fetal spleen	fetal spleen	spleen			pBluescript
Doods	(#937205)	<u> </u>				SK-
L0606	NCI_CGAP_Lym5	follicular lymphoma	lymph node			pBluescript
						SK-
L0608	Stratagene lung carcinoma	lung carcinoma	lung	NCI-H69		pBluescript
	937218				<u></u>	SK-
L0615	22 week old human fetal					pBluescriptII
	liver cDNA library					SK(-)
L0617	Chromosome 22 exon					pBluescriptII KS+
				<u> </u>		pBluescriptlI
L0618	Chromosome 9 exon				1	KS+
	G1 0 11			<u> </u>	 	pBluescriptII
L0619	Chromosome 9 exon II			ļ		KS+
L0622	HM1					pcDNAII
£0022	riivi i	1		ļ		(Invitrogen)
L0623	HM3	pectoral muscle				pcDNAII
L0023	111113	(after mastectomy)				(Invitrogen)
L0629	NCI_CGAP_Mel3	metastatic	bowel (skin			pCMV-
		melanoma to bowel	primary)			SPORT4
L0630	NCI_CGAP_CNS1	substantia nigra	brain	İ		pCMV-
				<u> </u>		sPORT4 pCMV-
L0631	NCI_CGAP_Br7		breast			SPORT4
						pCMV-
L0635	NCI_CGAP_PNS1	dorsal root ganglion	peripheral nervous			SPORT4
		!	system		1	
10626	NCI CGAP_Pit1	four pooled pituitary	brain			pCMV-
L0636	NCI_COAF_FILI	adenomas	0			SPORT6
L0637	NCI CGAP_Bm53	three pooled	brain			pCMV-
L0037	Nei_eg/ii _biiiss	meningiomas				SPORT6
L0638	NCI CGAP Brn35	tumor, 5 pooled (see	brain			pCMV-
50050		description)				SPORT6
L0639	NCI CGAP_Brn52	tumor, 5 pooled (see	brain			pCMV-
		description)		_		SPORT6
L0640	NCI_CGAP_Br18	four pooled high-	breast	1	Ì	pCMV- SPORT6
	·	grade tumors,	1	1	Į	3FOK 10
		including two prima		 	 	pCMV-
L0641	NCI_CGAP_Co17	juvenile granulosa	colon	1		SPORT6
1.25-	NGL CCAR Cale	tumor moderately	colon		 	pCMV-
L0642	NCI_CGAP_Co18	differentiated	201011		1	SPORT6
		adenocarcinoma			İ	
1.0643	NCL CGAP Co19		colon			pCMV-
L0643	NCI_CGAP_Co19	moderately	colon	L	_l	I pCIVI V -

	1	differentiated			SPORT6
		adenocarcinoma			
L0644	NCI_CGAP_Co20	moderately	colon		pCMV-
	1	differentiated		j	SPORT6
		adenocarcinoma			
L0645	NCI_CGAP_Co21	moderately	colon		pCMV-
		differentiated			SPORT6
		adenocarcinoma			
L0646	NCI_CGAP_Co14	moderately-	colon		pCMV-
	[differentiated	1		SPORT6
		adenocarcinoma			
L0647	NCI_CGAP_Sar4	five pooled	connective	,	pCMV-
		sarcomas, including	tissue		SPORT6
1.0648	NGL CCAR F2	myxoid liposarcoma squamous cell			pCMV-
L0648	NCI_CGAP_Eso2	carcinoma	esophagus		SPORT6
L0649	NCI CGAP_GUI	2 pooled high-grade	genitourinary		pCMV-
L0049	NCI_COAF_GOT	transitional cell	tract		SPORT6
		tumors	tract		·SIOKIO
L0650	NCI_CGAP_Kid13	2 pooled Wilms"	kidney		pCMV-
LUUJU	Noi_ed/ii_Ridis	tumors, one primary	Ridiley		SPORT6
		and one metast) Si Oktio
L0651	NCI CGAP Kid8	renal cell tumor	kidney		pCMV-
2000.					SPORT6
L0653	NCI_CGAP_Lu28	two pooled	lung		pCMV-
		squamous cell			SPORT6
		carcinomas	1		
L0654	NCI_CGAP_Lu31		lung, cell line		pCMV-
					SPORT6
L0655	NCI_CGAP_Lym12	lymphoma,	lymph node		pCMV-
		follicular mixed			SPORT6
		small and large cell			
L0656	NCI_CGAP_Ov38	normal epithelium	ovary		pCMV-
					SPORT6
L0657	NCI_CGAP_Ov23	tumor, 5 pooled (see	ovary		pCMV-
		description)			SPORT6
L0658	NCI_CGAP_Ov35	tumor, 5 pooled (see	ovary		pCMV-
	100.0018	description)			SPORT6
L0659	NCI_CGAP_Pan1	adenocarcinoma	pancreas	ļ	pCMV-
1.0661	NGL CCAP Malis		skin		SPORT6 pCMV-
L0661	NCI_CGAP_Mel15	malignant melanoma,	SKIN	}	SPORT6
		metastatic to lymph			SPORTO
		node	Í		ĺ
L0662	NCI_CGAP_Gas4	poorly differentiated	stomach		pCMV-
20002	1101_00711_0034	adenocarcinoma	Stornaen		SPORT6
		with signet r]		
L0663	NCI CGAP Ut2	moderately-	uterus		pCMV-
20005		differentiated			SPORT6
		endometrial			
		adenocarcino	l		
L0664	NCI_CGAP_Ut3	poorly-differentiated	uterus		pCMV-
		endometrial			SPORT6
		adenocarcinoma,			
L0665	NCI_CGAP_Ut4	serous papillary	uterus]	pCMV-
	1	carcinoma, high	ł		SPORT6
	1	1 amada 2 maalad t			
		grade, 2 pooled t			
L0666	NCI_CGAP_Ut1	well-differentiated	uterus		pCMV-
L0666	NCI_CGAP_Ut1	well-differentiated endometrial	uterus		pCMV- SPORT6
		well-differentiated endometrial adenocarcinoma, 7			SPORT6
L0666 L0667	NCI_CGAP_Ut1	well-differentiated endometrial	uterus whole blood		

			1		PGEM
L0697	Testis 1				5zf(+)
L0717	Gessler Wilms tumor				pSPORT1
L0731	Soares_pregnant_uterus_		uterus		pT7T3-Pac
	NbHPU				
L0738	Human colorectal cancer			<u> </u>	pT7T3D
L0740	Soares melanocyte	melanocyte			pT7T3D (Pharmacia)
1	2NbHM				with a
Ī	1				modified
-	1				polylinker
L0741	Soares adult brain		brain		pT7T3D
	N2b4HB55Y				(Pharmacia) with a
					modified
					polylinker
L0742	Soares adult brain		brain		pT7T3D
	N2b5HB55Y				(Pharmacia)
					with a modified
-					polylinker
L0743	Soares breast 2NbHBst		breast		pT7T3D
L0743	Soares oreast 214011BSt		0.000		(Pharmacia)
					with a
ļ				}	modified
	0 1 2271110		breast		polylinker pT7T3D
L0744	Soares breast 3NbHBst		breast		(Pharmacia)
	ŀ				with a
					modified
					polylinker
L0745	Soares retina N2b4HR	retina	eye		pT7T3D (Pharmacia)
					with a
				1	modified
	l				polylinker
L0746	Soares retina N2b5HR	retina	eye		pT7T3D
					(Pharmacia) with a
			1	1	modified
					polylinker
L0747	Soares fetal heart_NbHH		heart		pT7T3D
	19W				(Pharmacia)
					with a modified
	1				polylinker
L0748	Soares fetal liver spleen		Liver and	 	pT7T3D
20,40	1NFLS		Spleen		(Pharmacia)
					with a
		•			modified polylinker
1.0740	Soares_fetal_liver_spleen		Liver and	 	pT7T3D
L0749	_INFLS_SI		Spleen		(Pharmacia)
			•		with a
	,				modified
			1		polylinker
L0750			lung		(Pharmacia)
	yw				with a
				1	modified
				ļ	polylinker
L0751	Soares ovary tumor	ovarian tumor	ovary		pT7T3D (Pharmacia)
	I NIHOT		I	1 1	(Pharmacia) with a
L0750	Soares_fetal_lung_NbHL1 9W	ovarian tumor	lung		with a modification polyling pT7T3 (Pharm with a modification pT7T3 (Pharm (Pha

·					modified
	i				polylinker
10762	Soares_parathyroid_tumor	parathyroid tumor	parathyroid		pT7T3D
L0752		paratifyroid turnor	gland		(Pharmacia)
	_NbHPA		giand		with a
					modified
					polylinker
	- 1 1 1 2 2 2 2				pT7T3D
L0753	Soares_pineal_gland_N3H		pineal gland		(Pharmacia)
	PG			j	with a
]	modified
					polylinker
L0754	Soares placenta Nb2HP		placenta		pT7T3D
			ľ		(Pharmacia)
			4		with a
1					modified
					polylinker
L0755	Soares_placenta_8to9wee		placenta		pT7T3D
B0733	ks 2NbHP8to9W		•	i i	(Pharmacia)
	K8_21 (0.11 e e e)				with a
					modified
		!			polylinker
1.0756	Clainle caleregia	multiple sclerosis			pT7T3D
L0756	Soares_multiple_sclerosis _2NbHMSP	lesions			(Pharmacia)
	_2NDHMSP	iesions		ļ	with a
					modified
				ì	polylinker
					V_TYPE
		<u> </u>		 	pT7T3D
L0757	Soares_senescent_fibrobla	senescent fibroblast		1	(Pharmacia)
	sts_NbHSF			1	with a
					modified
				1	
				1	polylinker
					V_TYPE
L0758	Soares_testis_NHT		•		pT7T3D-Pac
	_			i 1	(Pharmacia)
				1	with a
					modified
					polylinker
L0759	Soares_total_fetus_Nb2H				pT7T3D-Pac
20.22	F8 9w	Ì			(Pharmacia)
	1.0_5	ļ			with a
		1		1	modified
	,				polylinker
L0761	NCI_CGAP_CLL1	B-cell, chronic			pT7T3D-Pac
LU/UI	1.000/11_00001	lymphotic leukemia			(Pharmacia)
	l	, ,p icakeima	1		with a
		1		1	modified
		1			polylinker
1.07/0	NGL CCAP P.1.1	breast	 	1	pT7T3D-Pac
L0762	NCI_CGAP_Br1.1	Ulcasi			(Pharmacia)
					with a
				1	modified
	1		1] !	polylinker
			 	 	pT7T3D-Pac
L0763	NCI_CGAP_Br2	breast	1	[(Pharmacia)
			1	1	with a
					modified
					polylinker
L0764	NCI_CGAP_Co3	colon			pT7T3D-Pac
			[(Pharmacia)
					with a
					modified polylinker

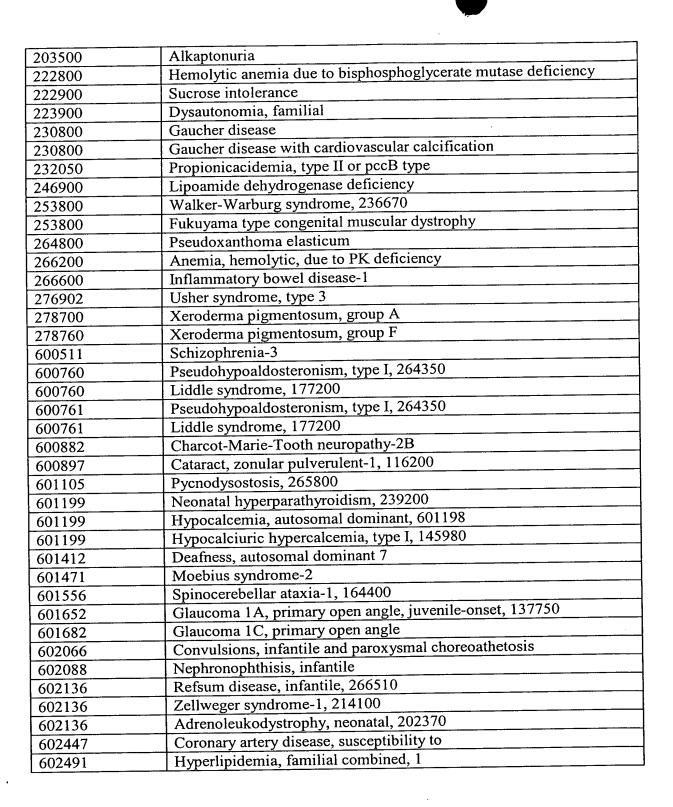
T 10766	Type coan cont	I		T	TTTID Dog
L0766	NCI_CGAP_GCB1	germinal center B cell			pT7T3D-Pac (Pharmacia)
		cen			with a
					modified
İ				1	polylinker
L0767	NCI_CGAP_GC3	pooled germ cell			pT7T3D-Pac
L0/0/	NCI_CGAP_GC3	tumors			(Pharmacia)
		tunors			with a
}					modified
					polylinker
L0768	NCI_CGAP_GC4	pooled germ cell			pT7T3D-Pac
20700	Nei_coni_de4	tumors			(Pharmacia)
1		14		1	with a
	1	1	:	l i	modified
		1			polylinker
L0769	NCI_CGAP_Brn25	anaplastic	brain		pT7T3D-Pac
20,03		oligodendroglioma	· · · · · · · · · · · · · · · · · · ·		(Pharmacia)
1				[with a
		1			modified
					polylinker
L0770	NCI_CGAP_Brn23	glioblastoma	brain		pT7T3D-Pac
~~~~		(pooled)			(Pharmacia)
		(,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			with a
					modified
				j j	polylinker
L0771	NCI_CGAP_Co8	adenocarcinoma	colon		pT7T3D-Pac
20,,,,	1.01_001000		55.5		(Pharmacia)
		<b> </b>			with a
				ļ į	modified
					polylinker
L0772	NCI_CGAP_Co10	colon tumor RER+	colon		pT7T3D-Pac
					(Pharmacia)
				İ	with a
		1			modified
					polylinker
L0773	NCI_CGAP_Co9	colon tumor RER+	colon		pT7T3D-Pac
1		<b>i</b>			(Pharmacia)
ĺ					with a
		1			modified
					polylinker
L0774	NCI_CGAP_Kid3		kidney		pT7T3D-Pac
				1 1	(Pharmacia)
					with a
1	ŀ				modified
					polylinker
L0775	NCI_CGAP_Kid5	2 pooled tumors	kidney		pT7T3D-Pac
1		(clear cell type)			(Pharmacia)
	1				with a
					modified
		<u> </u>			polylinker
L0776	NCI_CGAP_Lu5	carcinoid	lung		pT7T3D-Pac
	1			1	(Pharmacia)
}	1				with a
					modified
					polylinker
L0777	Soarcs_NhHMPu_S1	Pooled human	mixed (see		pT7T3D-Pac
1	1	melanocyte, fetal	below)		(Pharmacia)
		heart, and pregnant			with a modified
	[				
				ļ	polylinker
L0778	Barstead pancreas		pancreas		pT7T3D-Pac
	HPLRBI				(Pharmacia) with a
1					modified
L	<u></u>	_1	L	<u> </u>	modified

L0779 Soares_NFL_T_GBC_S1 pooled	polylinker pT7T3D-Pac (Pharmacia)
L0779   Soares_NFL_T_GBC_S1   pooled	
	with a
	3
	modified
	polylinker
L0780 Soares_NSF_F8_9W_OT pooled	pT7T3D-Pac
_PA_P_S1	(Pharmacia) with a
	modified
	polylinker
L0782 NCI_CGAP_Pr21 normal prostate prostate	pT7T3D-Pac
	(Pharmacia)
	with a modified
	polylinker
L0783 NCI_CGAP_Pr22 normal prostate prostate	pT7T3D-Pac
	(Pharmacia) with a
	modified
	I
	polylinker
L0785 Barstead spleen HPLRB2 spleen	pT7T3D-Pac
	(Pharmacia)
	with a modified
	3
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	polylinker
L0786 Soares_NbHFB whole brain	pT7T3D-Pac (Pharmacia)
	with a
	modified
	polylinker
LOTOT NOV COAD C. L.I	pT7T3D-Pac
L0787 NCI_CGAP_Sub1	(Pharmacia)
	with a
	modified
	polylinker
L0788 NCI CGAP Sub2	pT7T3D-Pac
L0788 NCI_CGAP_Sub2	(Pharmacia)
	with a
	modified
	polylinker
L0789 NCI_CGAP_Sub3	pT7T3D-Pac
101_CO/H_0400	(Pharmacia)
	with a
	modified
	polylinker
L0790 NCI_CGAP_Sub4	pT7T3D-Pac
30770 1101_00111_0001	(Pharmacia)
	with a
	modified
	polylinker
L0791 NCI_CGAP_Sub5	pT7T3D-Pac
	(Pharmacia)
	with a
	modified
	polylinker
L0792 NCI_CGAP_Sub6	pT7T3D-Pac
	(Pharmacia)
	with a
	modified
	polylinker
L0793 NCI_CGAP_Sub7	pT7T3D-Pac
·	(Pharmacia)
	with a

		·		·	modified
	ĺ				polylinker
		<del> </del>		ļ	pT7T3D-Pac
L0794	NCI_CGAP_GC6	pooled germ cell			(Pharmacia)
		tumors			with a
		1			
					modified
					polylinker
L0796	NCI_CGAP_Brn50	medulloblastoma	brain		pT7T3D-Pac
		1			(Pharmacia)
	i	1			with a
		1			modified
					polylinker
L0800	NCI_CGAP_Co16	colon tumor, RER+	colon		pT7T3D-Pac
	1				(Pharmacia)
				]	with a
	ļ	1			modified
					polylinker
L0803	NCI_CGAP_Kid11	1	kidney		pT7T3D-Pac
					(Pharmacia)
					with a
					modified
					polylinker
L0804	NCI_CGAP_Kid12	2 pooled tumors	kidney		pT7T3D-Pac
		(clear cell type)			(Pharmacia)
					with a
		-			modified
				ļ	polylinker
L0805	NCI_CGAP_Lu24	carcinoid	lung		pT7T3D-Pac
					(Pharmacia)
					with a modified
					polylinker
L0806	NCI_CGAP_Lu19	squamous cell	lung		pT7T3D-Pac
		carcinoma, poorly			(Pharmacia) with a
		differentiated (4			modified
	İ				polylinker
				<del> </del>	pT7T3D-Pac
L0807	NCI_CGAP_Ov18	fibrotheoma	ovary		(Pharmacia)
					with a
					modified
					polylinker
				<del> </del>	pT7T3D-Pac
L0808	Barstead prostate BPH		prostate		(Pharmacia)
	HPLRB4 1			1 1	with a
					modified
	·	1			polylinker
				<del> </del>	pT7T3D-Pac
L0809	NCI_CGAP_Pr28	Į Į	prostate		(Pharmacia)
					with a
		1			modified
					polylinker
			<u> </u>	<del> </del>	porymikei
L2251	Human fetal lung	Fetal lung			

## TABLE 5

OMIM	Description
Reference	
104770	Amyloidosis, secondary, susceptibility to
106165	Hypertension, essential, 145500
107670	Apolipoprotein A-II deficiency
108730	Brody myopathy, 601003
109400	Basal cell nevus syndrome
110700	Vivax malaria, susceptibility to
117700	[Hypoceruloplasminemia, hereditary]
117700	Hemosiderosis, systemic, due to aceruloplasminemia
125264	Leukemia, acute nonlymphocytic
126650	Chloride diarrhea, congenital, Finnish type, 214700
126650	Colon cancer
132800	Basal cell carcinoma
132800	Epithelioma, self-healing, squamous 1, Ferguson-Smith type
134570	Factor XIIIA deficiency
135940	Ichthyosis vulgaris, 146700
145001	Hyperparathyroidism-jaw tumor syndrome
146790	Lupus nephritis, susceptibility to
147781	Atopy, susceptibility to
150210	Lactoferrin-deficient neutrophils, 245480
150240	Cutis laxa, marfanoid neonatal type
152445	Vohwinkel syndrome, 124500
152445	Erythrokeratoderma, progressive symmetric, 602036
154276	Malignant hyperthermia susceptibility 3
159001	Muscular dystrophy, limb-girdle, type 1B
169600	Hailey-Hailey disease
172471	Glycogenosis, hepatic, autosomal
173360	Thrombophilia due to excessive plasminogen activator inhibitor
173360	Hemorrhagic diathesis due to PAI1 deficiency
174000	Medullary cystic kidney disease, AD
179755	Renal cell carcinoma, papillary, 1
180105	Retinitis pigmentosa-10
180380	Night blindness, congenital stationery, rhodopsin-related
180380	Retinitis pigmentosa, autosomal recessive
180380	Retinitis pigmentosa-4, autosomal dominant
182860	Pyropoikilocytosis
182860	Spherocytosis, recessive
182860	Elliptocytosis-2
186580	Arthrocutaneouveal granulomatosis
186855	Leukemia-2, T-cell acute lymphoblastic
190000	Atransferrinemia
191315	Insensitivity to pain, congenital, with anhidrosis, 256800



## Polynucleotide and Polypeptide Variants

- The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, nucleotide sequences encoding the polypeptide of SEQ ID NO:Y, the nucleotide sequence of SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A, the nucleotide sequence as defined in columns 8 and 9 of Table 2, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, the nucleotide sequence as defined in column 6 of Table 1B, nucleotide sequences encoding the polypeptide encoded by the nucleotide sequence as defined in column 6 of Table 1B, the cDNA sequence contained in Clone ID NO:Z, and/or nucleotide sequences encoding the polypeptide encoded by the cDNA sequence contained in Clone ID NO:Z.
- The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y, the polypeptide sequence as defined in column 7 of Table 1A, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the nucleotide sequence as defined in columns 8 and 9 of Table 2, a polypeptide sequence encoded by the nucleotide sequence as defined in column 6 of Table 1B, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA sequence contained in Clone ID NO:Z.
- [86] "Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.
- Thus, one aspect of the invention provides an isolated nucleic acid molecule comprising, or alternatively consisting of, a polynucleotide having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence described in SEQ ID NO:X or contained in the cDNA sequence of Clone ID NO:Z; (b) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) a nucleotide sequence in SEQ ID NO:X or the cDNA in Clone ID NO:Z which encodes a mature polypeptide; (d) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which encodes a biologically active fragment of a polypeptide;

(e) a nucleotide sequence in SEQ ID NO:X or the cDNA sequence of Clone ID NO:Z, which encodes an antigenic fragment of a polypeptide; (f) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (g) a nucleotide sequence encoding a mature polypeptide of the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (h) a nucleotide sequence encoding a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (i) a nucleotide sequence encoding an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (j) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), or (i) above.

The present invention is also directed to nucleic acid molecules which comprise, [88] or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i), or (j) above, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the cDNA contained in Clone ID NO:Z or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in Clone ID NO:Z, the nucleotide coding sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto, the nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, a nucleotide sequence encoding the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto, the nucleotide sequence in SEQ ID NO:X encoding the polypeptide sequence as defined in column 7 of Table 1A or the complementary strand thereto, nucleotide sequences encoding the polypeptide as defined in column 7 of Table 1A or the complementary strand thereto,

and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides and nucleic acids.

- [89] In a preferred embodiment, the invention encompasses nucleic acid molecules which comprise, or alternatively, consist of a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under lower stringency conditions, to a polynucleotide in (a), (b), (c), (d), (e), (f), (g), (h), or (i), above, as are polypeptides encoded by these polynucleotides. In another preferred embodiment, polynucleotides which hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.
- In another embodiment, the invention provides a purified protein comprising, or alternatively consisting of, a polypeptide having an amino acid sequence selected from the group consisting of: (a) the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; (b) the amino acid sequence of a mature form of a polypeptide having the amino acid sequence of SEQ ID NO:Y or the amino acid sequence encoded by the cDNA in Clone ID NO:Z; (c) the amino acid sequence of a biologically active fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Z; and (d) the amino acid sequence of an antigenic fragment of a polypeptide having the complete amino acid sequence of SEQ ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Y or the complete amino acid sequence encoded by the cDNA in Clone ID NO:Y.
- [91] The present invention is also directed to proteins which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, any of the amino acid sequences in (a), (b), (c), or (d), above, the amino acid sequence shown in SEQ ID NO:Y, the amino acid sequence encoded by the cDNA contained in Clone ID NO:Z, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X as defined in columns 8 and 9 of Table 2, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B, the amino acid sequence as defined in column 7 of Table 1A, an amino acid sequence encoded by the nucleotide

sequence in SEQ ID NO:X, and an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X. Fragments of these polypeptides are also provided (e.g., those fragments described herein). Further proteins encoded by polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these amino acid sequences under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are the polynucleotides encoding these proteins.

- By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence referred to in Table 1A or 2 as the ORF (open reading frame), or any fragment specified as described herein.
- [93] As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.
- [94] If the subject sequence is shorter than the query sequence because of 5' or 3'

deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

[95] For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

[96] By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to

5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

[97] As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence of a polypeptide referred to in Table 1A (e.g., the amino acid sequence identified in column 6) or Table 2 (e.g., the amino acid sequence of the polypeptide encoded by the polynucleotide sequence defined in columns 8 and 9 of Table 2) or a fragment thereof, the amino acid sequence of the polypeptide encoded by the polynucleotide sequence in SEO ID NO:B as defined in column 6 of Table 1B or a fragment thereof, the amino acid sequence of the polypeptide encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence of the polypeptide encoded by cDNA contained in Clone ID NO:Z, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237-245 (1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is expressed as percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

[98] If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding

subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

[99] For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the Nterminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

[100] The polynucleotide variants of the invention may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, polypeptide variants in which less than 50, less than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a

variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

[101] Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985)). These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. As an example, Ron et al. (J. Biol. Chem. 268: 2984-2988 (1993)) reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

[103] Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem. 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

[104] Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N-

or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

[105] Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptides of the invention. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, [106] 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, (e.g., encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); (3) Northern Blot analysis for detecting mRNA expression in specific tissues (e.g., normal or diseased tissues); and (4) in situ hybridization (e.g., histochemistry) for detecting mRNA expression in specific tissues (e.g., normal or diseased tissues).

[107] Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having functional activity. By a polypeptide having "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide of the invention for binding) to an anti-polypeptide of the invention antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention.

- [108] The functional activity of the polypeptides, and fragments, variants and derivatives of the invention, can be assayed by various methods.
- [109] For example, in one embodiment where one is assaying for the ability to bind or compete with a full-length polypeptide of the present invention for binding to an antipolypetide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as ELISA (enzyme linked immunosorbent assay), radioimmunoassays, "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.
- [110] In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, the ability of physiological correlates of a polypeptide of the present invention to bind to a substrate(s) of the polypeptide of the invention can be routinely assayed using techniques known in the art.
- [111] In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and fragments, variants and derivatives thereof to elicit polypeptide related biological activity (either *in vitro* or *in vivo*). Other methods will be known to the skilled artisan and are within the scope of the invention.
- [112] Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for

example, the nucleic acid sequence of the cDNA contained in Clone ID NO:Z, the nucleic acid sequence referred to in Table 1A (SEQ ID NO:X), the nucleic acid sequence disclosed in Table 2 (e.g., the nucleic acid sequence delineated in columns 8 and 9) or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

- [113] For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.
- [114] The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.
- [115] The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. See Cunningham and Wells, Science 244:1081-1085 (1989). The resulting mutant molecules can then be tested for biological activity.
- [116] As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For

example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly. Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitutions with one or more of the amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, serum albumin (preferably human serum albumin) or a fragment thereof, or leader or secretory sequence, or a sequence facilitating purification, or (v) fusion of the polypeptide with another compound, such as albumin (including but not limited to recombinant albumin (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)). Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

[117] For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. See Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).

[118] A further embodiment of the invention relates to polypeptides which comprise the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid

substitutions from a polypeptide sequence disclosed herein. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, an amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, an amino acid sequence encoded by the complement of SEQ ID NO:X, and/or an amino acid sequence encoded by cDNA contained in Clone ID NO:Z which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid substitutions.

In specific embodiments, the polypeptides of the invention comprise, or alternatively, consist of, fragments or variants of a reference amino acid sequence selected from: (a) the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein); (b) the amino acid sequence encoded by SEQ ID NO:X or fragments thereof; (c) the amino acid sequence encoded by the complement of SEQ ID NO:X or fragments thereof; (d) the amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or fragments thereof; and (e) the amino acid sequence encoded by cDNA contained in Clone ID NO:Z or fragments thereof; wherein the fragments or variants have 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, amino acid residue additions, substitutions, and/or deletions when compared to the reference amino acid sequence. In preferred embodiments, the amino acid substitutions are conservative. Polynucleotides encoding these polypeptides are also encompassed by the invention.

## Polynucleotide and Polypeptide Fragments

[120] The present invention is also directed to polynucleotide fragments of the polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers to a polynucleotide having a nucleic acid sequence which, for example: is a portion of the cDNA contained in Clone ID NO:Z or the complementary strand thereto; is a portion of the polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in Clone ID NO:Z or the complementary strand thereto; is a portion of a polynucleotide sequence encoding the amino acid sequence encoded by the region of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto; is a portion of the polynucleotide sequence of SEQ ID NO:X as defined in columns 8 and 9 of Table 2 or the complementary strand thereto; is

SEQ ID NO:X or the complementary strand thereto; is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X; is a polynucleotide sequence encoding a portion of a polypeptide encoded by the complement of the polynucleotide sequence in SEQ ID NO:X; is a portion of a polynucleotide sequence encoding the amino acid sequence encoded by the region of SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto; or is a portion of the polynucleotide sequence of SEQ ID NO:B as defined in column 6 of Table 1B or the complementary strand thereto.

The polynucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in Clone ID NO:Z, or the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 160, 170, 180, 190, 200, 250, 500, 600, 1000, or 2000 nucleotides in length ) are also encompassed by the invention.

[122] Moreover, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150, 4151-4200, 4201-4250, 4251-4300, 4301-4350, 4351-

4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 5851-5900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, 6151-6200, 6201-6250, 6251-6300, 6301-6350, 6351-6400, 6401-6450, 6451-6500, 6501-6550, 6551-6600, 6601-6650, 6651-6700, 6701-6750, 6751-6800, 6801-6850, 6851-6900, 6901-6950, 6951-7000, 7001-7050, 7051-7100, 7101-7150, 7151-7200, 7201-7250, 7251-7300 or 7301 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity). More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

[123] Further representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 601-650, 651-700, 701-750, 751-800, 801-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, 3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-3950, 3951-4000, 4001-4050, 4051-4100, 4101-4150, 4151-4200, 4201-4250, 4251-4300, 4301-4350, 4351-4400, 4401-4450, 4451-4500, 4501-4550, 4551-4600, 4601-4650, 4651-4700, 4701-4750, 4751-4800, 4801-4850, 4851-4900, 4901-4950, 4951-5000, 5001-5050, 5051-5100, 5101-5150, 5151-5200, 5201-5250, 5251-5300, 5301-5350, 5351-5400, 5401-5450, 5451-5500, 5501-5550, 5551-5600, 5601-5650, 5651-5700, 5701-5750, 5751-5800, 5801-5850, 58515900, 5901-5950, 5951-6000, 6001-6050, 6051-6100, 6101-6150, 6151-6200, 6201-6250, 6251-6300, 6301-6350, 6351-6400, 6401-6450, 6451-6500, 6501-6550, 6551-6600, 6601-6650, 6651-6700, 6701-6750, 6751-6800, 6801-6850, 6851-6900, 6901-6950, 6951-7000, 7001-7050, 7051-7100, 7101-7150, 7151-7200, 7201-7250, 7251-7300 or 7301 to the end of the cDNA sequence contained in Clone ID NO:Z, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity). More preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

[124] Moreover, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a nucleic acid sequence comprising one, two, three, four, five, six, seven, eight, nine, ten, or more of the above described polynucleotide fragments of the invention in combination with a polynucleotide sequence delineated in Table 1B column 6. Additional, representative examples of polynucleotide fragments of the invention comprise, or alternatively consist of, a nucleic acid sequence comprising one, two, three, four, five, six, seven, eight, nine, ten, or more of the above described polynucleotide fragments of the invention in combination with a polynucleotide sequence that is the complementary strand of a sequence delineated in column 6 of Table 1B. further embodiments, the above-described polynucleotide fragments of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotide fragments of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[127] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more fragments of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that

bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X (e.g., as described herein) are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[130] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[131] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower

stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In the present invention, a "polypeptide fragment" refers to an amino acid [132] sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the portion of SEQ ID NO:X as defined in columnns 8 and 9 of Table 2, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, a portion of an amino acid sequence encoded by the complement of the polynucleotide sequence in SEQ ID NO:X, and/or a portion of an amino acid sequence encoded by the cDNA contained in Clone ID NO:Z. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, 1361-1380, 1381-1400, 1401-1420, 1421-1440, or 1441 to the end of the coding region of cDNA and SEQ ID NO: Y. In a preferred embodiment, polypeptide fragments of the invention include, for example, fragments comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, 1361-1380, 1381-1400, 1401-1420, 1421-1440, or 1441 to the end of the coding region of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

[133] Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

[134] Accordingly, polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

[135] The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X or the complement thereof, a polypeptide encoded by

the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, a polypeptide encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1B, and/or a polypeptide encoded by the cDNA contained in Clone ID NO:Z). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y, or the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, a polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, and/or a polypeptide encoded by the cDNA contained in Clone ID NO:Z). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y and the polypeptide encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2), the cDNA contained in Clone ID NO:Z, and/or the complement thereof, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

[138] Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the

complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

[139] The present application is also directed to proteins containing polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a polypeptide sequence set forth herein. In preferred embodiments, the application is directed to proteins containing polypeptides at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to polypeptides having the amino acid sequence of the specific N- and C-terminal deletions. Polynucleotides encoding these polypeptides are also encompassed by the invention.

[140] Any polypeptide sequence encoded by, for example, the polynucleotide sequences set forth as SEQ ID NO:X or the complement thereof, (presented, for example, in Tables 1A and 2), the cDNA contained in Clone ID NO:Z, or the polynucleotide sequence as defined in column 6 of Table 1B, may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X (e.g., the polypeptide of SEQ ID NO:Y and the polypeptide encoded by the portion of SEQ ID NO:X as defined in columnns 8 and 9 of Table 2) or the cDNA contained in Clone ID NO:Z may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; http://www.dnastar.com/).

[141] Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions; Chou-Fasman alpha-regions, beta-regions, and turn-regions; Kyte-Doolittle hydrophilic regions and hydrophobic regions; Eisenberg alpha-and beta-amphipathic regions; Karplus-Schulz flexible regions; Emini surface-forming regions; and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

[142] Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

[143] Preferred polypeptide fragments of the invention are fragments comprising, or alternatively, consisting of, an amino acid sequence that displays a functional activity (e.g. biological activity) of the polypeptide sequence of which the amino acid sequence is a fragment. By a polypeptide displaying a "functional activity" is meant a polypeptide capable of one or more known functional activities associated with a full-length protein, such as, for example, biological activity, antigenicity, immunogenicity, and/or multimerization, as described herein.

[144] Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

[145] In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of: the polypeptide sequence shown in SEQ ID NO:Y; a polypeptide sequence encoded by SEQ ID NO:X or the complementary strand thereto; the polypeptide sequence encoded by the portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2; the polypeptide sequence encoded by the portion of SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereto; the polypeptide sequence encoded by the cDNA contained in Clone ID NO:Z; or the polypeptide sequence encoded by a polynucleotide that hybridizes to the sequence of SEQ ID NO:X, the complement of the

sequence of SEQ ID NO:X, the complement of a portion of SEQ ID NO:X as defined in columns 8 and 9 of Table 2, or the cDNA sequence contained in Clone ID NO:Z under stringent hybridization conditions or alternatively, under lower stringency hybridization as defined *supra*. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X, or a fragment thereof), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to the complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions defined *supra*.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described *infra*. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

[148] Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic

epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

[150] Non-limiting examples of epitopes of polypeptides that can be used to generate antibodies of the invention include a polypeptide comprising, or alternatively consisting of, at least one, two, three, four, five, six or more of the portion(s) of SEQ ID NO:Y specified in column 7 of Table 1A. These polypeptide fragments have been determined to bear antigenic epitopes of the proteins of the invention by the analysis of the Jameson-Wolf antigenic index which is included in the DNAStar suite of computer programs. By "comprise" it is intended that a polypeptide contains at least one, two, three, four, five, six or more of the portion(s) of SEQ ID NO:Y shown in column 7 of Table 1A, but it may contain additional flanking residues on either the amino or carboxyl termini of the recited Such additional flanking sequences are preferably sequences naturally found adjacent to the portion; i.e., contiguous sequence shown in SEQ ID NO:Y. The flanking sequence may, however, be sequences from a heterolgous polypeptide, such as from another protein described herein or from a heterologous polypeptide not described herein. In particular embodiments, epitope portions of a polypeptide of the invention comprise one, two, three, or more of the portions of SEQ ID NO:Y shown in column 7 of Table 1A.

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

[152] Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- Nhydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of antipeptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

[153] As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention (e.g., those comprising an immunogenic or antigenic epitope) can be fused to heterologous polypeptide sequences. For example, polypeptides of the present invention (including fragments or variants thereof), may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof, resulting in chimeric polypeptides. By way of another non-limiting example, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) may be fused with albumin (including but not limited to recombinant human serum albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)). In a preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with the mature form of human serum albumin (i.e.,

amino acids 1 – 585 of human serum albumin as shown in Figures 1 and 2 of EP Patent 0 322 094) which is herein incorporated by reference in its entirety. In another preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with polypeptide fragments comprising, or alternatively consisting of, amino acid residues 1-z of human serum albumin, where z is an integer from 369 to 419, as described in U.S. Patent 5,766,883 herein incorporated by reference in its entirety. Polypeptides and/or antibodies of the present invention (including fragments or variants thereof) may be fused to either the N- or C-terminal end of the heterologous protein (e.g., immunoglobulin Fc polypeptide or human serum albumin polypeptide). Polynucleotides encoding fusion proteins of the invention are also encompassed by the invention.

Such fusion proteins as those described above may facilitate purification and may [154] increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG fusion proteins that have a disulfidelinked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin (HA) tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, Proc. Natl. Acad. Sci. USA 88:8972-897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an aminoterminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni2+ nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

## Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

[156] Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

[157] In certain preferred embodiments, proteins of the invention are fusion proteins comprising an amino acid sequence that is an N and/or C- terminal deletion of a polypeptide of the invention. In preferred embodiments, the invention is directed to a fusion protein comprising an amino acid sequence that is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a polypeptide sequence of the invention. Polynucleotides encoding these proteins are also encompassed by the invention.

[158] Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

[159] As one of skill in the art will appreciate that, as discussed above, polypeptides of the present invention, and epitope-bearing fragments thereof, can be combined with heterologous polypeptide sequences. For example, the polypeptides of the present invention may be fused with heterologous polypeptide sequences, for example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM) or portions thereof (CH1, CH2, CH3, and any

combination thereof, including both entire domains and portions thereof), or albumin (including, but not limited to, native or recombinant human albumin or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999, EP Patent 0 413 622, and U.S. Patent No. 5,766,883, issued June 16, 1998, herein incorporated by reference in their entirety)), resulting in chimeric polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties (EP-A 0232 262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).

[160] Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a polypeptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., Cell 37:767 (1984)).

[161] Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999);

and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

[162] Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

## Recombinant and Synthetic Production of Polypeptides of the Invention

[163] The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by synthetic and recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

[164] The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

[165] The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon

at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

[166] As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418, glutamine synthase, or neomycin resistance for eukaryotic cell culture, and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178)); insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

[167] Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

[168] Vectors which use glutamine synthase (GS) or DHFR as the selectable markers can be amplified in the presence of the drugs methionine sulphoximine or methotrexate, respectively. An advantage of glutamine synthase based vectors are the availability of cell lines (e.g., the murine myeloma cell line, NS0) which are glutamine synthase negative. Glutamine synthase expression systems can also function in glutamine synthase expressing cells (e.g., Chinese Hamster Ovary (CHO) cells) by providing additional inhibitor to prevent the functioning of the endogenous gene. A glutamine synthase expression system and components thereof are detailed in PCT publications: WO87/04462; WO86/05807; WO89/01036; WO89/10404; and WO91/06657, which are hereby incorporated in their entireties by reference herein. Additionally, glutamine synthase expression vectors can be obtained from Lonza Biologics, Inc. (Portsmouth, NH). Expression and production of

monoclonal antibodies using a GS expression system in murine myeloma cells is described in Bebbington *et al.*, *Bio/technology* 10:169(1992) and in Biblia and Robinson *Biotechnol*. *Prog.* 11:1 (1995) which are herein incorporated by reference.

The present invention also relates to host cells containing the above-described [169] vector constructs described herein, and additionally encompasses host cells containing nucleotide sequences of the invention that are operably associated with one or more heterologous control regions (e.g., promoter and/or enhancer) using techniques known of in The host cell can be a higher eukaryotic cell, such as a mammalian cell (e.g., a human derived cell), or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. A host strain may be chosen which modulates the expression of the inserted gene sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically engineered polypeptide may Furthermore, different host cells have characteristics and specific be controlled. mechanisms for the translational and post-translational processing and modification (e.g., phosphorylation, cleavage) of proteins. Appropriate cell lines can be chosen to ensure the desired modifications and processing of the foreign protein expressed.

[170] Introduction of the nucleic acids and nucleic acid constructs of the invention into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., the coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., US Patent Number

5,641,670, issued June 24, 1997; International Publication Number WO 96/29411; International Publication Number WO 94/12650; Koller *et al.*, *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); and Zijlstra *et al.*, *Nature* 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

[172] Polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

[173] Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolization pathway is the oxidation of methanol to formaldehyde using  $O_2$ . This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for  $O_2$ . Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase

genes (AOXI) is highly active. In the presence of methanol, alcohol oxidase produced from the AOXI gene comprises up to approximately 30% of the total soluble protein in Pichia pastoris. See Ellis, S.B., et al., Mol. Cell. Biol. 5:1111-21 (1985); Koutz, P.J., et al., Yeast 5:167-77 (1989); Tschopp, J.F., et al., Nucl. Acids Res. 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the AOXI regulatory sequence is expressed at exceptionally high levels in Pichia yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

[177] In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

[178] In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with

polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

[179] In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., Nature, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the Disomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, tbutylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

[180] The invention encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

[181] Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include iodine (121 I, 123 I, 125 I, 131 I), carbon (14C), sulfur (35S), tritium (3H), indium (111 In, 112 In, 113 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 In, 115 I

In specific embodiments, a polypeptide of the present invention or fragment or variant thereof is attached to macrocyclic chelators that associate with radiometal ions, including but not limited to, ¹⁷⁷Lu, ⁹⁰Y, ¹⁶⁶Ho, and ¹⁵³Sm, to polypeptides. In a preferred embodiment, the radiometal ion associated with the macrocyclic chelators is 111 In. another preferred embodiment, the radiometal ion associated with the macrocyclic chelator ⁹⁰Y. the macrocyclic chelator 1,4,7,10is In specific embodiments, tetraazacyclododecane-N,N',N",N"'-tetraacetic acid (DOTA). In other specific embodiments, DOTA is attached to an antibody of the invention or fragment thereof via a linker molecule. Examples of linker molecules useful for conjugating DOTA to a polypeptide are commonly known in the art - see, for example, DeNardo et al., Clin Cancer Res. 4(10):2483-90 (1998); Peterson et al., Bioconjug. Chem. 10(4):553-7 (1999); and Zimmerman et al, Nucl. Med. Biol. 26(8):943-50 (1999); which are hereby incorporated by reference in their entirety.

[184] As mentioned, the proteins of the invention may be modified by either natural

processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Polypeptides of the invention may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic Modifications include acetylation, acylation, ADP-ribosylation, amidation, methods. covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[185] Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

[186] The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for

ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10,000, 10,500, 11,000, 11,500, 12,000, 12,500, 13,000, 13,500, 14,000, 14,500, 15,000, 15,500, 16,000, 16,500, 17,000, 17,500, 18,000, 18,500, 19,000, 19,500, 20,000, 25,000, 30,000, 35,000, 40,000, 45,000, 50,000, 55,000, 60,000, 65,000, 70,000, 75,000, 80,000, 85,000, 90,000, 95,000, or 100,000 kDa.

[187] As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo et al., Appl. Biochem. Biotechnol. 56:59-72 (1996); Vorobjev et al., Nucleosides Nucleotides 18:2745-2750 (1999); and Caliceti et al., Bioconjug. Chem. 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

[188] The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, such as, for example, the method disclosed in EP 0 401 384 (coupling PEG to G-CSF), herein incorporated by reference; see also Malik et al., Exp. Hematol. 20:1028-1035 (1992), reporting pegylation of GM-CSF using tresyl chloride. For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

[189] As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol